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INDENTIFICATION OF AN α -KETOGLUTARATE
ANALOGUE AS AN ANTICANCER AGENT

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ABSTRACT

Often correlated to a poor prognosis and increased mortality in cancer patients, hypoxic adaptation in tumors is mainly endorsed by Hypoxia Inducible Factor (HIF-1 α). Under conditions of oxygen scarcity, this transcription factor triggers the expression of specific target genes implicated in glycolysis, neoangiogenesis and survival. Although hypoxia signalling constitutes an interesting target, the development of therapeutics has been limited by the high rate of drug resistance.

We previously showed the lack of a respiratory Complex I causes the accumulation of α KG associated to destabilization of HIF-1 α that render cancer cells unable to adapt to hypoxia as a result of PHDs stimulation by their substrate α KG, ultimately resulting in a blocked tumor growth *in vivo*. This project aims to propose a selective metabolic approach based on the supplementation of α KG as an anticancer agent. To counter α KG limited permeability, the ketoacid was coupled to distinct hydrophobic carriers giving 7 ester analogues of α KG (α KGlogues) generated for the purpose of this study. The analogues were screened for their capacity to oppose to HIF-1 α stabilisation under hypoxic conditions and to selectively hamper cancer cells growth without marked toxicity on non-cancer counterparts. This approach allowed us to select α KG-PP as a potent and safe α KGlogue since it limits HIF-1 α stabilisation at long term, selectively impairs cancer cells proliferation and their *in vitro* tumorigenic properties while being well tolerated by the non-cancer counterparts. Further, a synergistic effect of the hydrophobic carrier, independent of HIF-1 α , was also unveiled. Metabolomics analysis revealed an intracellular peak in α KG upon treatment coupled to a rearrangement in other TCA cycle intermediates. α KG accumulation correlated with Raptor hyperphosphorylation at short-term, suggesting the α KGlogue mediates its effect through the block of mTORC1 signalling and protein synthesis. Finally, in the perspective of an α KG-based anticancer therapy, the selected analogue displayed anti-proliferative properties on 3D cancer spheroids and a *Drosophila melanogaster* cancer model. The present data highlight the safety and potency of the selected molecule both *in vitro* and *in vivo*, as well as the potential of α KG-based treatment to consider for future combinatory therapies to tackle cancer progression.

ABBREVIATIONS

2-HG: 2-hydroxyglutarate
5-hmC: 5-hydroxymethylcytosine
5fC: 5-formylcytosine
5caC : 5-carboxylcytosine
Ac-CoA : Acetyl-CoA
ALDA/ALDC: aldolase A and C
AML: Acute myeloide leukemias
AMPK: AMP activated kinase
Asn: Asparagine
ATP: Adenosine triphosphate
ARNT: Aryl Hydrocarbon Receptor nuclear translocator
BHD: Birt-Hogg-Dubé syndrome
bHLH-PAS: helix–loop–helix - per-arnt-sim
CI: Complex I
CA9: Carbonic anhydrase
CBP: CREB binding protein
ccRCC: Clear cell renal cell carcinoma
CH: Cysteine/histidine rich domain
CTAD: C-transactivation domain
DMSO: Dimethyl sulfoxide
EDTA: Ethylenediaminetetraacetic acid
EMT: Epithelial-to-mesenchymal transition
ETC: Electron transport chain
FA: Fumarate
FADH₂: Flavine adenine dinucleotide
FAO: Fatty acids β -oxidation
FH: Fumarate hydratase
FIH1: Factor inhibiting HIF
GAPDH: Glyceraldehyde 3-phosphate dehydrogenase
GBBH: γ -butyrobetain hydroxylase
GDH : Glutamate dehydrogenase
GLS: Glutaminase
GT: Glutamine transaminase
GOT: Glutamate oxaloacetate transaminases
GPT: Glutamate pyruvate transaminases
GLUT: Glucose transporter
GS: Glutamine synthase
HAPs: Hypoxia-activated-prodrugs
HDAC: Histone deacetylase
LC-MS: Liquid chromatography-Mass spectrometry
KMV: 3-methyl, 2-oxovaleric acid
HIF: Hypoxia inducible factor
His: Histidine
HK: Hexokinase
HRE: Hypoxia responsive element
IDH: isocitrate dehydrogenase

IGF: Insulin-like growth factor
 IMM: Inner mitochondrial membrane
 IMS: Inter-membrane mitochondrial space
 JmjC: Jumonji-containing domain
 JHDM: JmjC histone demethylases
 KDM: Lysine Demethylase
 LDHA: Lactate dehydrogenase A
 LZIP: Leucine-zipper domain
 MCT: Mono-lactate transporter
 MDH: Malate dehydrogenase
 MDM2: Mouse double minute 2
 mtDNA: Mitochondrial DNA
 MMPs: Metallo-proteinases
 mTOR: Mammalian/Mechanistic Target of rapamycin
 MTT: 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide
 nDNA: nuclear DNA
 NADH: Nicotinamide adenine dinucleotide
 NMLH: N-methyllysine hydroxylase
 NADPH: Nicotinamide adenine dinucleotide phosphate
 NTAD: N-transactivation domain
 OAA: Oxaloacetate
 ODDDs: Oxygen-degradation dependent domain
 OMM: Outer mitochondrial membrane
 OXPHOS: Oxidative phosphorylation
 P5C: Pyrroline-5-Carboxylate
 P4H: Proline 4(*R*)-hydroxylase
 PBS: Phosphate Buffer Saline
 PFK: Phosphofructokinase
 PKM2: Pyruvate Kinase M2
 PDK: Pyruvate dehydrogenase kinase
 PDH: Pyruvate dehydrogenase
 PHD: Prolyl hydroxylase
 Pro: Proline
 PVDF: Polyvinylidene fluoride
 pVHL: Von Hippel Lindau protein
 ROS: Reactive oxygen species
 SDS-PAGE : Sodium dodecyl sulfate polyacrylamide gel electrophoresis
 SA: Succinate
 SDH: succinate dehydrogenase
 SRB: Sulforhodamine B
 TBS: Tris Buffered Saline
 TCA: Trichloroacetic acid
 TCA cycle: Tricarboxylic acids cycle
 TETs: Ten Eleven Translocases
 TDG: Thymine-DNA glycosylase
 TLC: Thin Layer Chromatography
 TM-HIF: Triple-mutant HIF1A
 VDAC: Voltage-dependant anion channel
 VEGF: vascular endothelial growth factor
 WT: wild-type

α KG: α -ketoglutarate
 α KGDDs: α KG-dependent dioxygenases
 α KGDHC: α -ketoglutarate dehydrogenase complex
 α KG-G: α -ketoglutarate geraniol
 α KG-N: α -ketoglutarate nerol
 α KG-L: α -ketoglutarate linelol
 α KG-Cl: α -ketoglutarate 2, 4-dichloride
 α KG-tB: α -ketoglutarate terbutyl
 α KG-P: α -ketoglutarate phenyl
 α KG-PP: α -ketoglutarate diphenyl

INTRODUCTION

Hallmarks of cancer

Long thought to be a genetic disease, constant progress in understanding cancer biology now provide more insight into the multifactorial character of this burden. Malignant transformation occurs in a subset of neoplastic precursors as a result of genetic and epigenetic insults leading to uncontrolled expansion, to ultimately form complex tissues with a deranged architecture. A consistent body of evidence sustain that cancer onset happens as a succession of multiple processes (Hanahan and Weinberg 2000). Additionally, tumors are characterised by their high heterogeneity in terms of cellular population. Cancer cells were shown to actively cooperate with their recruited associated stromal cells and *vice versa* to foster tumor formation, progression and response to therapy. In this context, the diverse and complex characteristics that govern tumorigenesis have been elegantly stratified by Hanahan and Weinberg who defined 6 main capabilities as cancer cells hallmarks (Hanahan and Weinberg 2011). Through their progression towards malignancy cancer cells acquire the capacity to sustain proliferative signalling, to resist growth regulators and evade growth suppressors, they gain replicative immortality and resist cell death, and the whole culminates in cancer cells hyperproliferation. Further, to sustain this growth rate and the subsequent needs in nutrients and oxygen supply, cancer cells trigger continuous angiogenesis (angiogenic switch) leading to their characteristic anarchic vasculature. Lastly, malignancies gain invasive and migratory abilities following the loss of cell-cell and cell-ECM junctions or overexpression of pro-EMT transcription factors.

Moreover, recent knowledge permitted to index additional “enabling traits” represented by genomic instability and inflammation highlighting the contribution of the microenvironment to tumor progression (Hanahan and Weinberg 2011). Finally, two emerging hallmark capabilities further underline cancer cells ability to evade immune destruction and reprogram their metabolism. In this regard, cancer metabolism has gained tremendous interest in the past two decades allowing considerable progress in understanding the complexity of malignancies and amongst all to consider new approaches to better tackle them.

Mitochondria: cellular hub for metabolic and bioenergetic reactions

Far from their bacterial origins, mitochondria constitute important organelles that occupy a central role in many cellular processes. Next to cellular respiration, they are also involved in programmed cell death, calcium-homeostasis and stress response. As semi-independent organelles, mitochondria carry their own genetic material and translation machinery contained in the mitochondrial matrix (MM) (Friedman and Nunnari 2014). Mitochondrial DNA (mtDNA) is a double stranded circular molecule of 16,569 base pair that encodes for 13 proteins of the total proteins the organelle counts, the rest being encoded by nuclear DNA (nDNA), synthesised in the cytoplasm then imported to the mitochondria. mtDNA displays some peculiarities that distinguish it from genomic DNA: in addition to being deprived of protective histones or a DNA repair system, mitochondrial DNA is maternally inherited and can exist in multiple copies in a single organelle (polyploidy). Hence, a condition of homoplasmy (wild-type or mutant) thus exists when all mtDNA copies are identical. By opposition, the co-existence of two mitogenomes (wild-type and mutant) in a single cell defines a heteroplasmic state. In a general manner, a heteroplasmic mutation translates at the phenotypic level beyond a defined threshold (usually between 70-90% mutation load). In addition, the homo/heteroplasmy (mutation load) levels is also influenced by mitotic segregation as mitochondria and thus mtDNA molecules are randomly segregated during mitosis.

The countenance of the MM is englobed by the inner mitochondrial membrane (IMM), known for its highly restricted permeability. A second, more permeable membrane wraps up the inner mitochondrial membrane thereby creating a space in between: the intermembrane mitochondrial space (IMS) (Frey and Mannella 2000). The IMM forms invaginations or “cristae” within the mitochondrial matrix which density directly reflects tissue energetic needs. At the functional level, mitochondria are important players involved in a plethora of reactions both in cellular bioenergetic and metabolism. Following glycolysis-derived pyruvate conversion to Acetyl Co-A (Ac-CoA) in the mitochondrial matrix, the latter is coupled to oxaloacetate and engages in the tricarboxylic acids (TCA) cycle reactions. Deeply anchored into the inner mitochondrial membrane IMM, reside the respiratory chain complexes or electron transport chain (ETC) (Khulbrandt et al., 2015). From complex I to complex IV, the enzymatic giants insure oxidative phosphorylation of reducing equivalents (NADH, FADH₂) produced by the TCA cycle, electron transport and proton pumping to the IMS space thus creating an electrochemical gradient necessary for ATP synthesis by F₀ F₁-

ATP-synthase or complex V that together with other 4 complexes of ETC formed the oxidative phosphorylation (OXPHOS). Besides glucose metabolism, mitochondria are at the heart of many other catabolic processes (Fatty acids β -oxidation, glutamine and branched-amino acids) as well as biosynthetic reactions including nucleotides, amino acids, fatty acids and heme synthesis. Finally, the organelles are also indispensable for metabolic by-products elimination (urea cycle, ROS) (Spinelli and Haigis 2018).

Mitochondria and metabolic reprogramming in cancer

Because of their central position in cellular metabolism and energy production, since the mid-90s mitochondria have gained growing interest for their contribution to key steps of tumorigenesis (initiation, progression and metastasis). Indeed, numerous studies demonstrate the active implication of the organelles as modulators of metabolic and hypoxic adaptations characterising cancer cells thereby sustaining their uncontrolled proliferation and growth into tumors (Porporato et al., 2018).

In cancer cells, glycolysis and TCA cycle intermediates are deviated from their initial purposes. Instead of energy production, they are mainly used to provide the necessary precursors for biosynthesis of macromolecules (proteins, lipids, nucleic acids) in order to support proliferation. In this frame, Otto Warburg was the first to note that cancer cells preferably use glucose as an energy source to release lactate thereby concluding to a possible mitochondrial aberration. Later, further studies demonstrated that cancer cells rewire their metabolism from oxidative to glycolytic independently from their mitochondrial efficiency (Smolková et al., 2011). Indeed, despite the low energy yield glycolysis allows (2 ATP molecules vs. 36 from oxidative phosphorylation), it seems to rather constitute a more favourable alternative for fastly proliferating cancer cells (Lunt and Vander Heiden 2011). In this regard, glucose being the most abundant nutrient in the extracellular space, cancer cells augment their glucose consumption rate by upregulating the expression of glucose transporters and glycolytic enzymes as a result of oncogenes-mediated stimulation (DeBerardinis et al., 2008) (Lunt and Vander Heiden 2011). Another advantage of the glycolytic pathway is that it provides cancer cells with the precursors necessary for macromolecules biosynthesis such as pyruvate and citrate for *de novo* lipid synthesis, NADPH and ribose sugars for nucleotide synthesis (DeBerardinis et al., 2008).

On the other hand, glutamine is the most abundant amino acid available to cancer cells. It therefore plays an important role in carbon and nitrogen metabolism. In this frame, glutaminolysis constitutes an anaplerotic pathway that refills the TCA cycle with α -ketoglutarate (α KG). In fast proliferating cells, it constitutes a new entry point to the cycle as a result of glucose shifting from oxidative phosphorylation (DeBerardinis et al., 2007). Moreover, several studies demonstrate that glutamine-derived α KG, undergo mitochondrial reductive carboxylation as the main carbon source to support the growth of cancer cells bearing mitochondrial defects or submitted to low oxygen conditions (Fendt et al. 2013) (Mullen et al., 2012) (Wise et al., 2011) (Metallo et al., 2012). The ketoacid is converted to citrate through an isocitrate dehydrogenases IDH1/IDH2-dependent reaction (Wise et al., 2011) (Metallo et al., 2012). Part of the citrate generated is used to sustain lipogenesis through Ac-CoA, on the one hand, and to replenish the pool of TCA cycle with oxaloacetate (OAA) and other intermediates. Paradoxically, a portion of the glutamine-derived α KG still engages in the oxidative TCA cycle pathway in order to generate reducing equivalents (Mullen et al., 2014). Therefore, even though the main energy sources are rearranged in cancer cells, it is now clear that the co-existence of both glycolytic and oxidative/reductive metabolisms all of which are complimentary to sustain cancer cells high growth rate (Zheng et al., 2012).

HIFs signalling and hypoxic adaptation in cancer

Hypoxia Inducible Factors (HIFs) are heterodimeric transcription factors of the basic-helix-loop-helix-PER-ARNT-SIM (bHLH-PAS) family (Wang et al., 1995). At the structural level, the transcription factors include a constitutively expressed nuclear-subunit β (Aryl Hydrocarbon Receptor nuclear translocator, ARNT) and an oxygen-labile subunit α which expression is tightly regulated by oxygen availability. In mammals, subunit β counts two described isoforms, respectively ARNT (or HIF-1 β) and ARNT2, while three paralogues of the α subunit have been described so far, HIF-1 α , HIF-2 α and HIF-3 α . HIF-1 α and HIF-2 α are the best characterised and structurally similar. HIF-3 α presents distinct structural features (Yang et al., 2015) (Figure 1) and can exist as different spliced variants some of which were reported to negatively regulate HIF-1 α and HIF-2 α activity (Makino et al., 2001). In addition to their bHLHL and PAS domains, HIFs structures encompass N- and C-transactivation domains (N-TAD, C-TAD). In addition, subunits alpha specifically harbours an overlapping oxygen-dependent degradation domain (ODDD) (Figure 1). HIF-1 α is ubiquitously expressed in mammalian cells whereas HIF-2 α and HIF-3 α expression is selectively restricted to some

tissues (Ema et al., 1997) (Yang et al., 2015). HIF-1 α paralogs were also identified in other lower organisms, for instance in *C. elegans* as well as in *Drosophila*. Similar is the corresponding paralogue thus suggesting the conservation of HIF system in all organisms (Semenza 2012).

Under low oxygen tension (0.1-5% O₂), subunits α escape oxygen-dependent degradation, translocate to the nucleus where their heterodimerization with subunit β occurs through a complex interaction involving the proteins respective bHLH and PAS-A domains (Jiang et al., 1996). The complex formation allows further interaction with a core DNA sequence (G/ACGTG) located in the Hypoxia Response Element (HRE) in the promoter region of HIF target genes, thereby triggering their transcription. Conversely, in high oxygen tension (5-21% O₂) subunits α are rapidly degraded (half-life <5minutes) through a complex oxygen-dependent enzymatic cascade. HIF sensing is mediated by post-translational modifications at the level of two proline residues located within the ODDD of subunits α (Figure 1). Prolines 402 and Pro564 for HIF-1 α or Pro405 and Pro531 for HIF-2 α undergo a 4-*trans*-hydroxylation catalysed by Fe(II)/ α KG-dependent dioxygenases (α KGDDs), namely prolyl hydroxylases containing domain (PHDs) (Jaakkola et al., 2001) (Ivan et al., 2001). As members of the α KGDDs family, the activity of the dioxygenases is allosterically regulated by the levels of TCA cycle intermediate α -ketoglutarate (α KG). Conversely, HIF-3 α possesses one single proline hydroxylation site in its ODDD. This step is necessary for further recognition and binding by von Hippel-Lindau (pVHL) tumor suppressor protein of the E3 ubiquitin ligase complex (Yu et al., 2001). HIF α subunits are subsequently polyubiquitinated and targeted to proteasomal degradation. HIF signalling is further controlled by another post-translational modification catalysed by a distinct enzyme of the α KGDDs family, namely Factor Inhibiting HIF (FIH1) which interferes with its transcriptional activity. In this regard, FIH1 catalyses a β -hydroxylation of an asparagine (Asn) residue located in the hypoxia protein C-TAD domain (Asn803 for HIF-1 α and Asn851 for HIF-2 α) thereby impeding its interaction and subsequent binding to cysteine/histidine-rich domain (CH1) domain of p300/CBP transcriptional co-activator (Mahon et al., 2001) (Lando 2002) (McNeill et al., 2002) (Figure 1). This mechanism thus constitutes an additional O₂-dependent checkpoint to control HIF pathway. Next to the canonical oxygen-dependent regulation, HIF-1 α stability, transcriptional and translational expression can be modulated by different effectors following non-canonical mechanisms especially in the context of cancer

(Iommarini et al., 2017). Amongst these non-canonical effectors are oncometabolites, which will be described in detail in the next section.

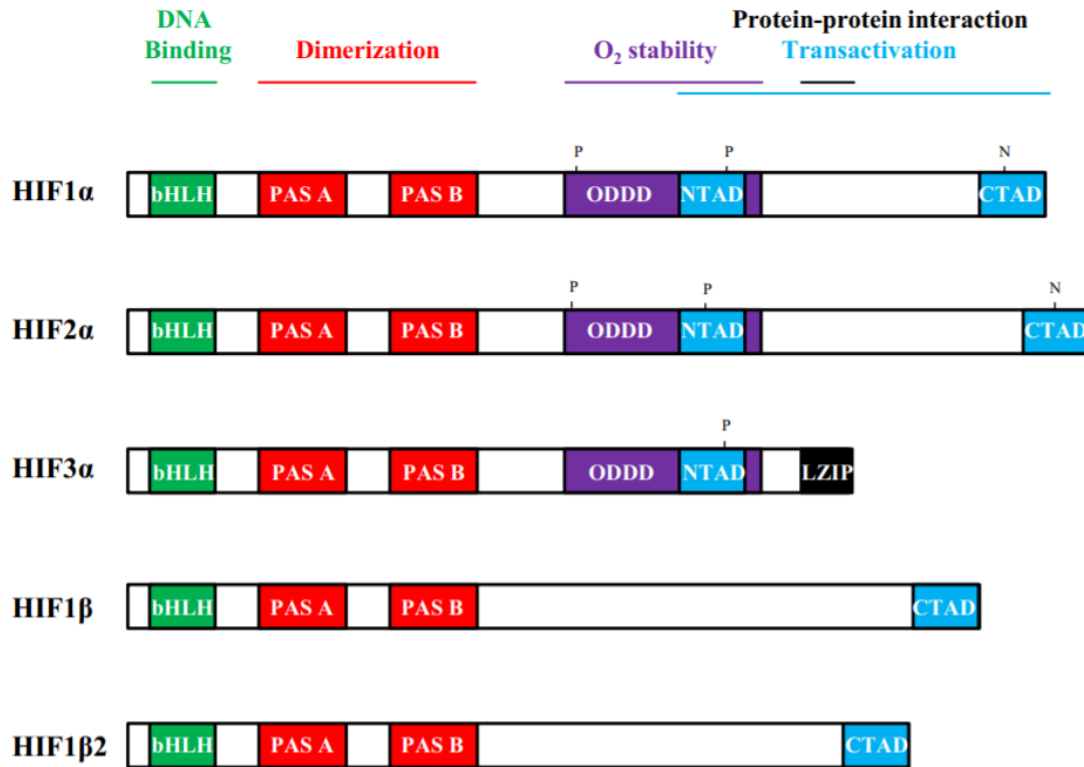


Figure 1: Schematic representation of HIFs structural domains and their corresponding roles (Ravenna et al., 2015). Each motif is represented in a different colour. All HIF isoforms bear a basic-Helix-Loop-Helix (bHLH) and a tandem PER-ARNT-SIM (PAS-A, PAS-B) domain necessary for DNA binding and subunits heterodimerization, respectively. HIF α subunits harbour an N-Transactivation Domain (NTAD) located within the oxygen-dependent-degradation domain (ODDD). This latter is site for oxygen-dependent post-translational hydroxylation of two proline residues (for HIF-1 α and HIF-2 α) by prolyl hydroxylases ultimately targeting the subunits for proteasomal degradation. By contrast, HIF-3 α includes a single proline residue for hydroxylation. HIF-1 α and HIF-2 α structures also comprise a C-transactivation domain (CTAD) determining for the protein transcriptional activity. In this domain resides an asparagine residue site for FIH1-catalysed hydroxylation. Instead, HIF-3 α possesses a Leucine-zipper domain (LZIP) involved in protein-protein interaction. Oxygen-insensitive HIF β subunits are deprived of ODDD and bear a single CTAD. P: Proline residue, N: Asparagine residue. *Permission to reuse allowed*

As described earlier, cancer cells preferably rewire their metabolism towards aerobic glycolysis even in high oxygen conditions. However, tumor organisation due to uncontrolled growth and microenvironment pressure all result in chronic HIF signalling especially in the

tumors innermost parts. HIF activation orchestrates cell adaptation to low oxygen availability in order to sustain cell survival in such extreme conditions. In this frame, the transcription factor counts amongst its numerous targets many pro-glycolytic genes. It mediates an increase in glucose consumption rates by upregulating glucose transporters GLUT1, GLUT3 (Semenza et al., 2012). Similarly, it stimulates the expression of different glycolytic enzymes including hexokinases 1 and 2 (HK1, HK2), phosphofructokinase (PFK1, PFK2), aldolase A and C (ALDA, ALDC), Pyruvate Kinase M2 (PKM2). Pyruvate dehydrogenase kinases (PDK1, PDK3) (Kim et al., 2006) are also upregulated by hypoxia resulting in pyruvate dehydrogenase (PDH) inactivation thereby opposing to pyruvate engaging into the TCA cycle and favouring its conversion to lactate. Consequently, lactate dehydrogenase A (LDHA) as well as mono-lactate transporters (MCT1, MCT4) expression is upregulated in hypoxia along with carbonic anhydrase (CA9). The latter enzyme contributes in concert with MCT transporters to insure H^+ efflux thereby inducing intracellular alkalinisation and extracellular acidification reported to promote invasion (Figure 2) (Semenza et al., 2012). In line with this, HIF stimulates the expression of metallo-proteinases (MMP-2, -9, -14) and extracellular matrix remodelling further enhancing cancer cells metastatic potential (Semenza et al., 2012). As an adaptative factor for oxygen restriction, HIFs stimulates angiogenesis through the increased transcription of angiogenic growth factors including VEGF to enhance vessel formation thereby sustaining one of cancer hallmarks (Figure 2) (Semenza et al., 2012). Further, hypoxia was reported to downregulate oxygen consumption along with ETC activity (Papandreou et al., 2006) (Masson and Ratcliffe 2014) while promoting the expression of glutamine dehydrogenase (GDH) likely to stimulate glutamine-dependent anaplerosis (Jiang et al., 2017). In these conditions glutamine reductive carboxylation is preferably used by cancer cells to sustain fatty acid and lipids synthesis as a consequence of pyruvate rewiring from the mitochondria (Wise et al., 2011) (Metallo et al. 2012). Finally, by eliciting the activation of repressor genes *SNAIL*, *SNAIL2*, *ZEB1*, *ZEB2*, HIF is also involved in epithelial-to-mesenchymal transition (EMT) (Unwith et al., 2015) (Semenza et al., 2012) and regulates several genes involved in stemness, cell immortalisation, genomic instability and therapy resistance (Unwith et al., 2015).

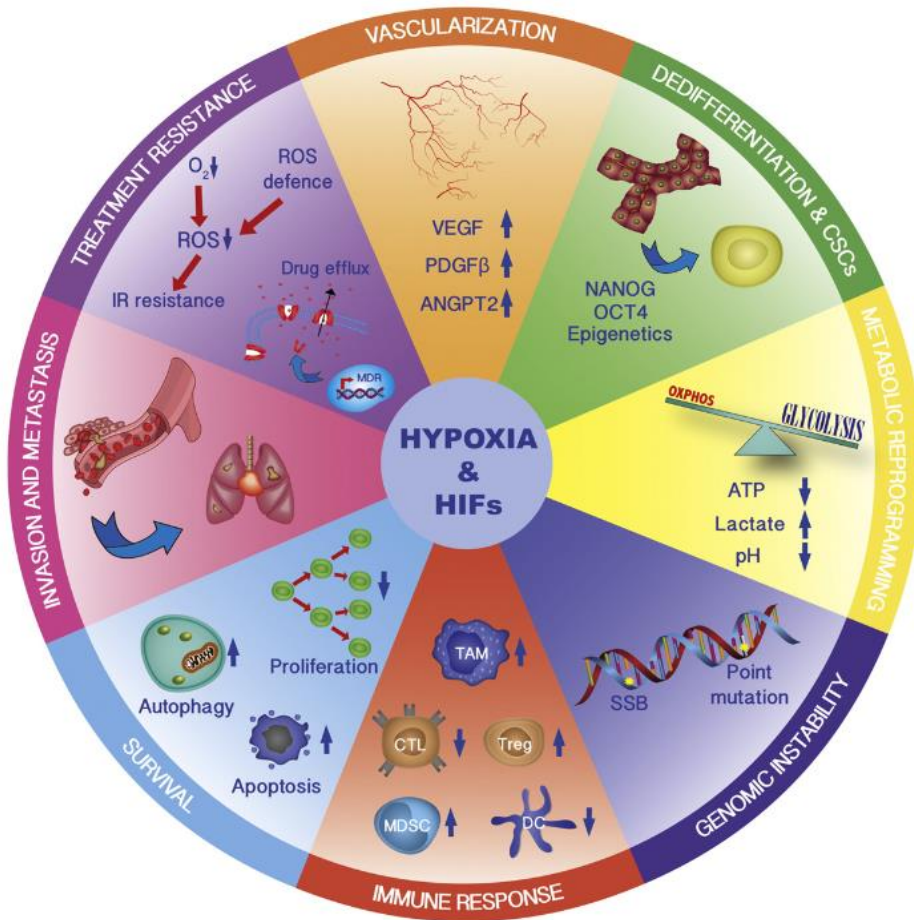


Figure 2: HIF signalling and cancer hallmarks: beyond metabolic adaptation (Wigerup et al., 2016). Through a wide range of targets, the activation of chronic hypoxic signalling promotes multiple processes that ultimately contribute to sustain cancer progression, metastasis and resistance to therapy. *Permission to reuse allowed*

Oncometabolites contribution to cancer progression

Succinate dehydrogenase (SDH), fumarate hydratase (FH) and isocitrate dehydrogenases (IDH1 and IDH2) are considered as tumor suppressors since loss of function mutations affecting these TCA cycle enzymes were reported in different types of cancers. The subsequent accumulation of substrate metabolites, namely succinate (SA), fumarate (FA) and 2-hydroxyglutrate (2-HG) was demonstrated to play an active role in oncogenic signaling, thereby classifying them as oncometabolites (Sciacovelli and Frezza 2016). Loss of function mutations in SDH genes have been reported in hereditary paraganglioma and pheochromocytoma, renal cell carcinoma, gastrointestinal stromal tumors and T-cell leukemia (Niemann and Müller, 2000) (Vanharanta et al., 2004) (Stratakis et al., 2009) (Baysal et al., 2007). On the other hand, FH was found mutated in hereditary leiomyomatosis and

renal cell carcinoma, paraganglioma and pheochromocytoma, clear cell carcinoma and neuroblastoma (Tomlinson et al., 2002) (Castro-Vega et al., 2014), whereas heterozygous somatic mutations affecting IDH1 and IDH2 were reported in gliomas and acute myeloid leukemias (AML) (Yan et al., 2009)(Mardis et al., 2009). In the latter case, the resulting arginine replacement (R132 in IDH1 and R172 or 140 in IDH2), provokes a shift in the enzyme's substrate affinity (Yang et al., 2010) and the gain of an NADPH-dependent neomorphic function leading to α KG reduction to (*R*)-2-hydroxyglutarate (D-2-HG) (Dang et al., 2009) (Ward et al., 2010). Notably, 2-HG generation by wild-type IDH2 was also reported during glutamine reductive carboxylation in cancer cells submitted to hypoxia (<1% O₂) (Wise et al., 2011). Since 2-HG is a chiral molecule, the existence of an L-2-HG isomer has also been reported in human cancer cells bearing defects in mitochondrial respiratory chain (Mullen et al., 2012) or as a result of promiscuous activity of LDHA and malate dehydrogenase (MDH) under hypoxic conditions (Intlekofer et al., 2015) (Intlekofer et al., 2017). At the structural level, SA, FA, D-2-HG and L-2-HG are very close to α KG. Such structure analogy allows oncometabolites to competitively inhibit the activity of α KG-dependent dioxygenases by occupying the enzyme's catalytic site, with different levels of potency (Koivunen et al., 2007) (Xu et al., 2011). As members of the α KG-dependent dioxygenases family (α KGDDs), PHDs and FIH1 constitute privileged targets for the oncometabolites. In this regard, inhibition of PHDs following SA and FA accumulation was shown to block HIF-1 α degradation in normal oxygen conditions, thereby inducing a state of pseudohypoxia *in vitro* and *in vivo* cancer models (Pollard et al., 2005) (Selak et al., 2005) (Isaacs et al. 2005). Although their effect on PHDs is still debated, both D- and L-2-HG markedly reduced FIH-dependent hydroxylation of HIF-1 α , explaining in part the high levels of the hypoxia protein observed in IDH-mutated cancers (Zhao et al., 2009) (Chowdhury et al., 2011).

Genetic instability is a hallmark of cancer (Hanahan and Weinberg 2011). In line with this, epigenetic aberrations have also been widely described in cancers (Esteller et al., 2008). They are even thought to precede classical transforming events as in the case of tumor suppressors genes. Indeed, cancer cells show genome wide hypomethylation, CpG islands promoter hypermethylation, as well as histone modification, all converging to genomic instability (Esteller et al., 2008). The dynamic character of epigenetic modifications and the tight interplay with cellular metabolism altogether play a part in malignant transformation. In this regard, the implication of oncometabolites in the modulation of this aspect has been widely

studied, most likely by altering the activity of Ten Eleven Translocases (TETs) family of DNA 5-methylcytosine hydroxylases and Histone Lysine demethylases (KDMs) both members of the α KGDDs superfamily. In this frame, several studies linked supra-physiological levels of SA, FA or 2-HG with repressed activity of TET hydroxylases and KDMs in various cancer subtypes (Xiao et al., 2012) (Xu et al., 2011) (Shim et al., 2014) (Laukka et al., 2016) (Chowdhury et al., 2011). A further illustration of this detrimental effect was the hypermethylated phenotype displayed by SDH and FH-deficient tumors (Letouzé et al., 2013) (Loriot et al., 2015) (Sciacovelli et al., 2016) as well as in IDH-mutated models (Figuerola et al., 2010) (Turcan et al., 2012) (Xu et al., 2011). Accordingly, pathological levels of SA, FA and 2-HG promoted EMT activation in cancer cell models (Loriot et al., 2015) (Sciacovelli et al., 2016) (Grassian et al., 2012) (Colvin et al., 2016) strongly confirming their pro-tumorigenic activity. In particular, 2-HG was also reported to block cell differentiation in hematopoietic cells (Figuerola et al., 2010) (Losman et al., 2013) (Lu et al., 2012), thereby supporting the pro-leukemogenic role of this oncometabolite.

However, the inhibition exerted by oncometabolites on α KGDDs family members was shown to be reversible considering its competitive nature. This can be achieved by modulating α KG/oncometabolite ratio through α KG supplementation (Xu et al., 2011) (MacKenzie et al., 2007) (Tennant et al., 2009).

α KG: a metabolite with pleiotropic activity

α KG at the heart of physiological reactions

α KG, or 2-oxoglutarate (2OG) is a tricarboxylic acid composed of 5 carbons with two weak carboxylic functions and a ketone group in the α position. Within the TCA cycle, IDH3 produces α KG through an irreversible reaction taking place in the mitochondria and where NAD^+ is limiting (Plaut et al., 1983). Wild-type IDH1 and IDH2 normally catalyse the reversible NADP^+ -dependent oxidative decarboxylation of isocitrate to either in the cytosol (IDH1) or in the mitochondria (IDH2). As a precursor of glutamine, the ketoacid can also originate from glutaminase (GLS)-mediated glutaminolysis and subsequent glutamate deamination by glutamate dehydrogenase (GDH) (Figure 3). Conversely, the reaction catalysed by GDH being reversible, transamination of α KG by GDH forms glutamate, which further amination by glutamine synthase (GS) gives glutamine. Furthermore, an additional reaction mediated by cytosolic or mitochondrial ω -amidase, particularly reported in

mammalian liver and kidney, can also generate α KG as follows: glutamine transamination by glutamine transaminase (GT) first produces an intermediate ketoacid: α -ketoglutaramate, which subsequent hydrolysis by α -amidase releases α KG and ammonia (Cooper et al., 2016). Hence, through the glutamine- α KG axis, the ketoacid is tightly involved in amino acids metabolism, an anabolic pathway of particular importance especially in cancer cells (Xiao et al., 2016). Likewise, glutamate pyruvate transaminases (GPT1/2) and glutamate oxaloacetate transaminases (GOT1/2 cytoplasmic and mitochondrial respectively) respectively produce α KG from glutamate and pyruvate or oxaloacetate transamination reactions (Figure 3). (Sookoian et al., 2015). Like most of the TCA cycle intermediates, α KG diffuses from the mitochondrial matrix to the cytoplasm and vice-versa. It crosses the inner mitochondrial membrane through a 2-oxoglutarate-malate antiporter and the outer mitochondrial membrane through voltage-dependant anion channel (VDAC) (Monné et al., 2013).

Owing to its metabolic origin and structure, α KG is found at the centre of a wide range of physiological processes qualifying it as pleiotropic molecule (Abla et al., 2020). First of all, both glutamine and α KG have an anabolic role on protein synthesis since glutaminolysis increases intracellular glutamate pools which will be used together with α KG as precursors in transamination reactions for proline, arginine, ornithine amino acids synthesis. The two latter amino acids are known to stimulate growth factors release such as growth hormone (GH) and Insulin-like growth factor (IGF) (Harrison and Pierzynowski, 2008). Clinical studies also reported benefits of α KG alone or in combination (with ornithine or arginine) both in animals and in humans on protein synthesis, muscle mass and body weight gain in post-operative, -trauma patients or those suffering from extensive burns, but also in malnourished aging patients (Zdzisińska et al., 2017). Further, many studies related positive effects of α KG on bone tissue formation suggesting the metabolite to have an anabolic effect and inhibit bone resorption *in vivo* (Zdzisińska et al., 2017). Secondly, α KG structure confers the metabolite a high reactivity. Indeed, with its two carboxylic and ketone groups, α KG is capable of neutralising hydrogen peroxide (H_2O_2) through non-enzymatic oxidative decarboxylation thus preventing oxidative stress damage in mammalian and *Drosophila melanogaster* models (Long et al., 2011) (Bayliak et al., 2015). α KG was also described to neutralise ammonia and ethanol-induced oxidative stress as well as for its antidote effect in case of cyanide poisoning (Abla et al., 2020).

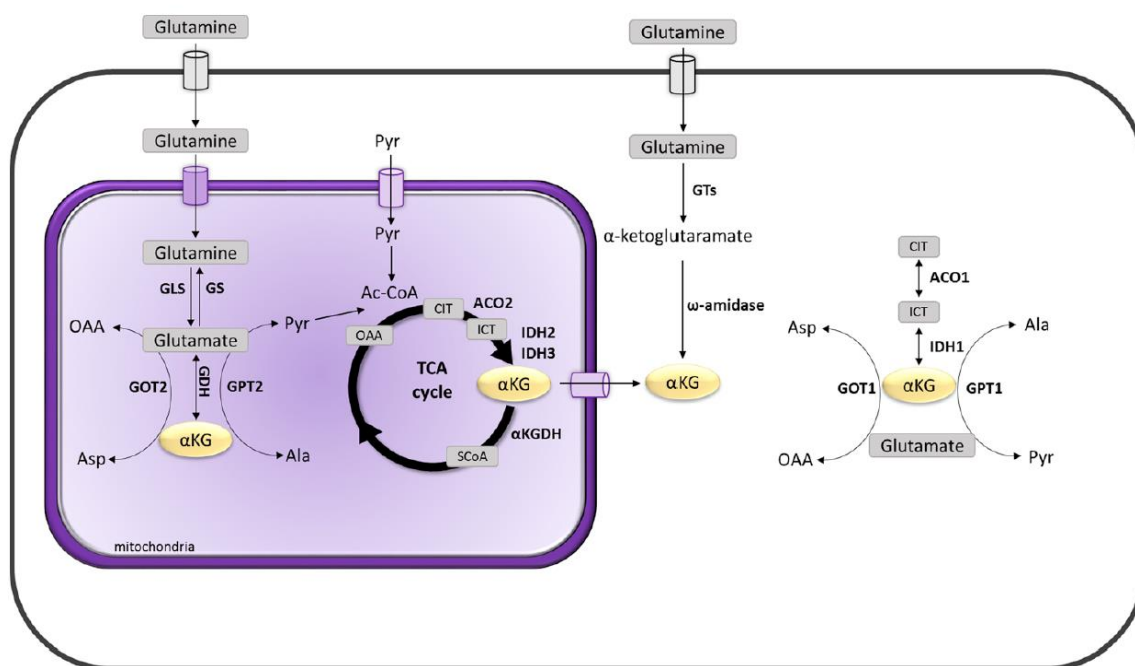


Figure 3: αKG biosynthetic pathways (Abla et al., 2020). αKG derives from glutamine and glutamate deamination in the mitochondria, mediated by glutaminase (GLS) and glutamate dehydrogenase (GDH), respectively. In the cytosol, glutamine transamination by glutamine transaminases (GTs), generates α-ketoglutarate that is subsequently converted into αKG by an ω-amidase. Moreover, αKG can originate from transamination of glutamine by GTs or glutamate by GPT1/GOT1, in the presence of Pyr/OAA respectively. Inside the mitochondria, GPT2 and GOT2 isoforms catalyze the same reactions. Lastly, the conversion of TCA cycle intermediate isocitrate catalyzed by isocitrate dehydrogenases IDH2 and IDH3 in the mitochondria or IDH1 in the cytosol constitutes another source of αKG

The processes of metabolism and aging being tightly related, dietary restrictions and pharmacological modulation of energy metabolism were previously described to benefit longevity although the underlying molecular mechanisms are still not clearly defined. As aging is often coupled to events like genomic instability, telomere shortening, epigenetic alterations, through its metabolic properties αKG seems to display a beneficial effect in reversing or delaying such alterations. In this frame, Chin and colleagues showed that αKG was able to inhibit ATP synthase β-subunit in *C. elegans*, resulting in increased lifespan and autophagy induction through the inhibition of TOR signalling (Chin et al., 2014). In continuity with this, the metabolite delivered as calcium salt similarly increased lifespan, survival and age-related morbidities reducing different negative factors such as inflammation in female mice (Shahmirzadi et al., 2019). Interestingly, αKG was also correlated to

pluripotency maintenance in mice embryonic stem cells by promoting histone and DNA demethylation (Carey et al., 2015).

α KG as a limiting substrate for dioxygenases

In addition to bridging energy and amino acid metabolisms, the ketoacid is at the crossroads of biological events orchestrated by the super-family of α KGDDs enzymes. Being the dioxygenases obligate substrate, the enzymes use α KG along with iron and ascorbate to catalyse hydroxylation reactions on specific residues of their target proteins while releasing succinate as in the regulation of HIF levels by PHDs or during the early phases of nucleic acids *N*-demethylation endorsed by TET family enzymes.

α KGDDs constitute a widespread family of phylogenetically conserved enzymes harbouring the same fold and requiring α KG as well as a non-haem iron for their catalytic activity. In humans, these enzymes display affinity for various types of substrates ranging from amino acid residues, nucleic acids to metabolic intermediates (Markolovic et al., 2015). At the structural level, *bona fide* α KGDDs share the same double-stranded β -helix (DSBH) fold, also common to the Jumonji C (JmjC) chromatin-associated proteins. The DSBH core is made of 8 antiparallel β -strands (I–VIII), that fold two by two in a helical manner (β -helix) to form two distorted β -sheets conferring to the enzymes a characteristic distorted barrel structure at the end of which reside the active site with iron/metal and α KG binding pockets (Islam et al., 2018). α KG dioxygenases catalyse a two-electron oxidation hydroxylation reaction of their respective substrates through the sequential binding of ferrous iron, α KG followed by O_2 and substrate. Binding of each respective substrate implies interactions with specific amino-acid residues and coordination sites occupied by 6 water molecules (Schofield and Ratcliffe 2004). First, iron binding to the active site is enabled by interaction with a highly conserved amino-acid triad (facial triad) that constitute the iron Fe(II)-binding motif (Figure 4). Facial triad typically presents as a *HX(D/E)...H* motif and include a proximal and a distal histidine residues (respectively located in the β -II and β -VII strands), while the third residue was mainly reported to be an aspartate (Hegg and Jr 1997). Then, two coordination sites occupied by two water molecules are subsequently displaced to allow α KG binding. The ketoacid chelates Fe^{2+} in a bidentate manner via its C-1 carboxylate and ketone oxygen, thereby forming an octahedral complex (Figure 4). Further electrostatic interactions between its C-5 carboxylate and a basic residue as well as a neutral side chain residue allow binding stabilisation (Markolovic et al., 2015). This step is followed by substrate binding and

subsequent uncovering of the final coordination site favouring oxygen binding. α KG oxidative decarboxylation produces succinate, carbon dioxide and a water molecule along with a ferryl intermediate (FeIV_O) (Figure 4) which reacts with substrate C-H to form the hydroxylated product, while Fe(IV) is reduced to Fe(II). At the term of the reaction, the hydroxylated product is first released followed by succinate (Islam et al., 2018). Of note that some, but not all α KGDDs also necessitate the presence of ascorbate which seems to mainly stand an antioxidant role protecting the iron metal from oxidation.

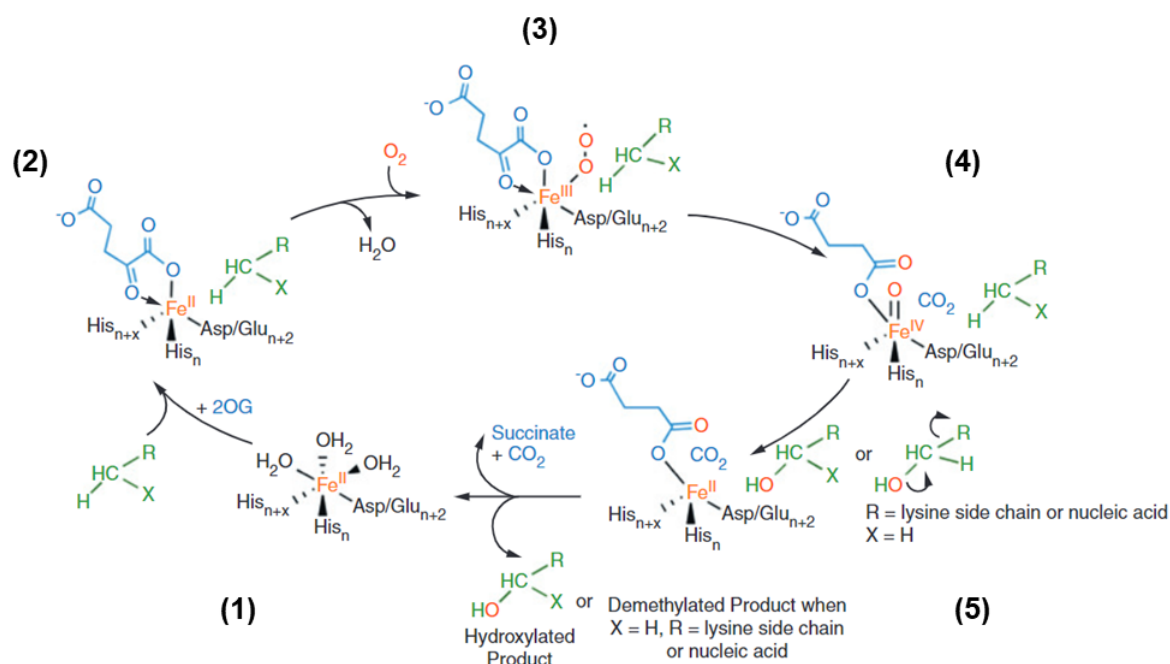


Figure 4: Mechanism of α KG-dependent dioxygenases catalysed hydroxylation (Adapted from (Aik et al., 2012)). First, iron binds to the active site following interaction with the amino-acids facial triad (1). Then, two coordination sites occupied by two water molecules are displaced to allow α KG binding. The ketoacid chelates Fe^{2+} in a bidentate manner thereby forming an octahedral complex (2). This step is followed by substrate binding (2) and subsequent uncovering of the final coordination site favouring oxygen binding (3). α KG oxidative decarboxylation produces succinate, carbon dioxide and a water molecule along with a ferryl intermediate (FeIV_O) (4) which reacts with the substrate to form the hydroxylated product, while Fe(IV) is reduced to Fe(II) (5). The hydroxylated product is first released followed by succinate (5). *Permission to reuse allowed*

Amongst the α KGDDs super-family, prolyl hydroxylases (PHDs) are the most important and the best described members, because of their role in hypoxia sensing. Displaying very high affinity for molecular oxygen with K_m values in the range of 100-250 μM , these enzymes thus constitute notable oxygen sensors (Kaelin and Ratcliffe 2008). To date, three PHD paralogues

have been described so far: PHD1, PHD2 and PHD3 (also known as EglN2, EglN1 and EglN3 respectively, the orthologues of Egl-9 in *C. elegans*) (Epstein et al., 2001) (Ivan et al., 2002) although a fourth isoform has also been reported (Kaelin and Ratcliffe 2008). At the cellular level, PHD1 was shown to exclusively locate in the nucleus while PHD2 is cytoplasmic and PHD3 was found in both sub-cellular compartments (Metzen et al., 2003). In addition to oxygen sensing and HIF regulation, some PHDs were reported to be involved in additional cellular processes. For instance, PHD1 and PHD3 have been reported to have growth suppressive effects (Erez et al., 2003) (Fong and Takeda, 2008). Presenting with the lowest K_m for O_2 , studies in mammalian cells have shown that HIF-1 α levels are mainly regulated by PHD2 in normoxia and PHD1 to a lesser extent (Berra et al., 2003). By contrast, PHD1 preferably acts on HIF-2 α , while PHD3 displays affinity only for HIF-2 α C-TAD (Appelhoff et al., 2004) (Ivan and Kaelin 2017). Although altogether, the process of HIF regulation seems to be more intricate and mainly dependent on the cellular context as well as expression levels of each respective isoform (Ivan and Kaelin 2017). Interestingly, PHD2 and PHD3 but not PHD1 expression was described to be stimulated by hypoxia suggesting the existence of a negative feedback control on HIF signalling (Berra et al., 2003). FIH1, for which a single isoform has been described so far, presents a different sequence to PHDs and further structural and computational studies identified the enzyme with a Jumonji homology region thereby classifying it in a distinct subfamily of α KGDDs (Hewitson et al., 2002) (Lando et al., 2002). FIH1 displays a K_m value of 90 μ M for O_2 (Koivunen et al., 2004). Likewise, to carry on their catalytic activity, PHDs and FIH1 are strictly dependent on α KG intracellular amounts with K_m values of 50 μ M and 25 μ M, respectively, suggesting the enzymes activity can be influenced by the slightest fluctuations in the ketoacid levels (Table 1) (Koivunen et al., 2004). As a matter of fact, it can also be modulated by the levels α KG of structural analogues, namely succinate which constitutes the product of the HIF-hydroxylating enzymes along with other oncometabolites (FA and 2-HG) (Table 1). In this frame, fumarate was described to be the most potent in negatively modulating PHDs dioxygenase activity (Koivunen et al., 2007) followed by succinate, thereby giving more insights into their role as oncometabolites. Citrate, oxaloacetate and pyruvate also displayed the ability to interfere with PHDs and FIH1 with different levels of potency. The latter seems to be more sensitive to citrate and oxaloacetate competitive binding (Koivunen et al., 2007). It is important to note that the reported values are calculated on recombinant enzymes. Thus, the situation *in vivo* is more dynamic and directly depends on multiple additional factors.

K_m (μ M)				IC_{50} (μ M)			
2OGGDs	Fe^{2+}	2OG	O_2	Succinate	Fumarate	R-2HG	S-2HG
EGLN1	0.05	1-270	65-250	510	80	300	240-1,150
EGLN2	0.05	2	230	830	120	210	630
EGLN3	0.1	10	230	570	60	-	90
FIH1	0.5	25-150	90-240	>10,000	>10,000	1,100-1,500	190-300
P4HA1	2	20	40	190	400	1800	310
TET1	5	55	0.3-30	390	540	4000	1,000
TET2	4	60	0.5-30	400	570	5000	1,600

Table 1: K_m and IC_{50} values of α KGDDs for their co-substrates and α KG structural analogues (Adapted from (Losman et al., 2020)).

Eukaryotic chromatin is organised in basic units, namely nucleosomes. Nucleosome structure comprises an octamer of core histones (H2A, H2B, H3 and H4) around which is wrapped a 147 bp DNA segment. Chromatin core histones can undergo numerous post-translational modifications (methylation, acetylation, phosphorylation, ubiquitylation and SUMOylation) at the level of their free tails. In particular, methylation span at lysine and arginine residues. Histone modifications directly reflect the state of chromatin folding (euchromatin vs. heterochromatin) hence giving insight on transcriptional activation or repression. Long considered as static, histone methylation landscape seems to define a histone code that is read and interpreted by adapted proteins (Pedersen and Helin 2010). DNA and histone tails epigenetic modifications play an important role in the regulation of transcription regulation, genome integrity and cell fate.

Enzymes of the Ten Eleven Translocase family are dioxygenases known to catalyse active DNA-demethylation by oxidising 5-methylcytosine (5mC) in CpG rich islands of genes promoters (Tahiliani et al., 2009). This process takes place in a multiple step reaction that successively gives rise to 5-hydroxymethylcytosine (5-hmC), 5-formylcytosine (5fC) then 5-carboxylcytosine (5caC) ultimately leading to base-excision by Thymine-DNA glycosylase (TDG) (Ito et al., 2011) (He et al., 2011). There are known 3 TET isoforms, TET1-TET3 all of which display the typical double-stranded β -helix fold characterising α KGDDs (Wu and Zhang 2017). As a member of Fe(II)/ α KG-dependent dioxygenases, TETs-catalysed reaction on DNA requires the presence of both substrates for optimal activity. Likewise, the activity of the enzymes is also sensitive to oxygen availability (Table 1).

In parallel, chromatin-associated Jumonji-containing domain proteins (JmjC) represent the largest class of demethylases and belong to the α KGDDs family thanks to structural similarities with other members of the super-family. These proteins, also known as JmjC histone demethylases (JHDM) or Lysine Demethylases (KMDs) thus harbour a JumonjiC (JmjC) domain and are capable of catalysing histone demethylation through oxidative decarboxylation of α KG in the presence of O₂ and Fe(II) (Tsukada et al., 2006). As stated in previous sections, both TETs and KDMs are sensitive to competitive inhibition by oncometabolite 2-HG (Xu et al., 2011), both 2-HG enantiomers acting as weak competitive inhibitors and reversibly occupying the enzymes catalytic site (Laukka et al., 2016) (Xu et al., 2011).

Next to its role in oxygen-dependent HIF degradation and epigenetic regulation of gene expression, α KG is also involved in the synthesis and crosslinking of collagen fibers, the major component of connective tissues (Figure 5). Collagen strains are composed of amino acids triplet Xaa-Yaa-Gly, where Xaa is usually (2S)-proline, Yaa, (2S,4R)-hydroxyproline and Glycine residues. Collagen fibers are stabilised under the effect of two types of α KG-dependent dioxygenases: proline 4(R)-hydroxylase (P4H), which catalyse stereospecific *trans* prolyl 4-hydroxylation of the proline residue in the Yaa position (Gorres and Raines 2010), and proline 3(S)-hydroxylases which catalyse prolyl-3-hydroxylation, at Xaa position. By its chemical properties *trans* 4-hydroxyproline stabilizes collagen polypeptides. This step is necessary for subsequent folding of collagen triple helixes thus setting the pavement to other post-translational modifications. Like other OGDs, P4H requires substrates α KG and O₂, Fe(II) and ascorbic acid as a cofactor to reduce iron. The lack of ascorbate causes the development of scurvy disease secondary to prolyl hydroxylase inactivity and thus collagen instability.

Moreover, α KG pleiotropic position also involves it in L-carnitine biosynthesis thereby in lipid metabolism, by serving as a substrate for N-methyllysine hydroxylase (NMLH) and γ -butyrobetain hydroxylase (GBBH). Both enzymes of α KGDDs family respectively catalyse the first and last step of L-carnitine synthesis, a cofactor that insures the import of long chain fatty acids into the mitochondria for β -oxidation (Vaz and Wanders 2002). On the other hand, α KG and PHD1 were reported to modulate NF- κ B signalling cascade implicated in inflammatory response to cytokines, cell survival and proliferation observed in tumorigenesis. Cummins and colleagues (Cummins et al., 2006) demonstrated that inactivation of IKK β kinase following an oxygen-dependent hydroxylation of a proline

residue (P191) is mediated by PHD1 (Figure 5). IKK β is known to activate NF- κ B after phosphorylating Inhibitory κ B- α (IkB- α), thus uncovering the transcription factor's Nuclear Localisation Sequences in hypoxic conditions.

In conclusion, shedding light on the multiple implications of α KG in all the above-mentioned metabolic, epigenetic and regulatory processes gives a general view of multiple virtues the ketoacid can offer in the scope of developing potential therapeutic applications.

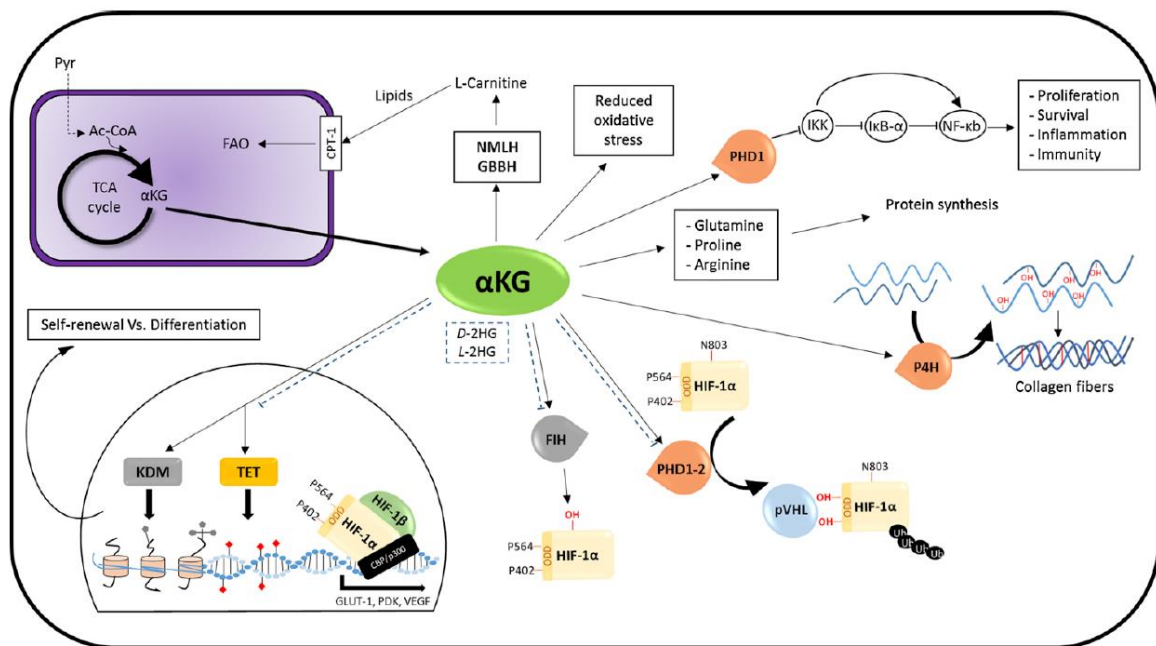


Figure 5: Pleiotropic implication of α KG in cell homeostasis (Abla et al., 2020). α KG is involved in multiple cellular processes both in physiological and pathological contexts. It protects against oxidative stress, modulates protein and lipid biosynthesis, and is involved in fatty acids β -oxidation (FAO). As substrate of α KG dependent dioxygenases, it activates hydroxylases (PHDs and FIH1) to limit HIF-1 α signalling, leading to pVHL-mediated protein poly-ubiquitination and proteasomal degradation in normoxia. The metabolite also affects gene expression and cell stemness by promoting epigenetic DNA and histone demethylation by TETs and KDMs enzymes. Finally, α KG stimulates PHD1 to inactivate NF- κ B signalling and is likewise determining in the process of collagen monomers stabilization.

Targeting hypoxic adaption as a therapeutic strategy in cancer

Tumor hypoxia in solid tumors often correlates with a poor prognosis and increased mortality in cancer patients (Vaupel et al., 2001) (Bertout et al., 2008). The activation of HIF

signalling, or hypoxic adaptation is well documented to confer an aggressive phenotype coupled to chemo- and radiotherapy resistance as a result of an uncontrolled tumor growth and aberrant vascular architecture (Vaupel et al., 2001) (Bertout et al., 2008). Consequently, a great interest had arisen to tackle HIF pathway in neoplasms through direct or indirect approaches.

HIF inhibitors

One class of compounds developed to target hypoxia signalling are Hypoxia-activated-prodrugs (HAPs). These inactive compounds engineered to be converted into their active pharmacological forms in a hypoxic environment following enzymatic activation present thus the advantage of target specificity. Often designed to target DNA replication, many of these prodrugs are being presently tested in clinical trials (Phillips et al., 2016). Next to that, a wide range of molecules have been reported in literature for their ability to antagonise HIFs heterodimerisation, DNA-binding and transcriptional activity or mRNA expression. In this frame, acriflavine binds PAS domains of HIF-1 α and HIF-2 α subunits and was shown to potently reduce tumor growth and vascularization in xenograft models (Lee et al., 2009). Similarly, PT2385 which displays a higher affinity for HIF-2 α subunit is being investigated in clinical trials in patients with ccRCC renal cell carcinomas (Chen et al., 2016). In the class of compounds blocking HIF-1 α transcriptional activity, Bortezomib, a proteasome inhibitor already approved for the treatment of multiple myeloma, reportedly stimulated HIF-dependent repression of HIF-1 α transcriptional activity. However, when used as a single therapy the drug lacked potency in colorectal cancer patients cohorts (Mackay et al., 2005). In the same class, molecules of the chetomin family were not pursued because of toxicity issues despite their ability to repress HIF-p300 interaction. In the category of candidates opposing to HIF-DNA binding, despite showing interesting effects on VEGF expression *in vitro*, both polyamides and echinomycin were not as potent in clinical trials and were thus not pursued. Finally, the largest part of compounds described so far are those blocking HIF mRNA translation or protein expression and potentially the most promising. In this scope, an interesting candidate is EZN-2698. An RNA antagonist reported for its ability to specifically inhibit the expression of HIF-1 α mRNA levels and its target genes correlating with reduced tumor growth *in vitro* and *in vivo* (Greenberger et al., 2008). In clinical trials this compound showed promising effects in patients with renal cell carcinoma (Wigerup et al., 2016). Within the class of topoisomerase inhibitors, camptothecin analogue, namely topotecan was able to downmodulate HIF-1 α translation and protein levels resulting in reduced tumor growth in

xenograft models (Rapisarda et al., 2009). Further, irinotecan as well as its active metabolite (SN38) displayed low toxicity levels and encouraging results in Phase I clinical trials in patients with brain tumors (Norris et al., 2014). In addition, compounds opposing to HIF stabilisation which have been approved or are currently investigated in clinical studies, include histone deacetylase (HDAC) inhibitors (Romidepsin and trichostatin) as well as Heat-shock protein 90 (Hsp90) inhibitors (Masoud and Li, 2015). In the frame of an indirect approach, drugs targeting signalling pathways upstream of HIF are also under investigation. Indeed, it is well known that HIF-1 α mRNA levels are upregulated by PI3K/AKT/mTOR pathway, hence molecules modulating with this pathway can constitute an interesting alternative. Amongst mTOR inhibitors, Temsirolimus stands out as the most promising as it passed phase II clinical trial and is now approved by the FDA for the treatment of metastatic renal cell carcinoma (Revaud et al., 2010) (Batelli and Cho, 2011).

Although considerable efforts have been invested in developing HIF-targeted therapies, the high rate of therapy resistance hints to the necessity of combining approaches in order to enhance treatment success chances. In this frame, it is important to note that the severe alteration of mitochondrial CI activity has been correlated to chronic HIF-1 α destabilisation subsequently blocking tumor growth *in vitro* and *in vivo* (Kurelac et al., 2019).

Targeting mitochondrial CI in cancer

Respiratory complex I (CI) or NADH:ubiquinone oxidoreductase is the largest protein of the ETC with its 44 subunits, 7 of which (ND1-6 and ND4L) are encoded by mtDNA. The remaining 37 subunits are encoded by nDNA then imported into the mitochondria where they assemble into a functional enzyme. This finely tuned process involves different chaperone proteins (Guerrero Castillo et al., 2017). Mitochondrial CI plays a key role in energy homeostasis and is similarly involved in the maintenance of redox balance as well as in cellular processes like apoptosis. The protein heads the ETC to catalyse the oxidation of TCA cycle-derived NADH thereby transferring 2 electrons to ubiquinone while pumping two protons into the mitochondrial intermembrane space thereby generating an electrochemical gradient and contributing to the ATP production by F₀-F₁ ATP-synthase.

Despite the great deal of studies reporting mitochondrial mutations spanning in CI subunits in many cancers, such mutations are unlikely able to trigger oncogenic transformation *per se*. Nonetheless, the contribution of the mtDNA mutations in CI genes in the process of oncogenesis, cancer progression, metastasis and therapy resistance has been widely debated

(Leone et al. 2018), and lately further investigations allowed to stratify the pathogenicity of such defects depending on: i. the mutation type, ii. the mutation load or threshold (Giuseppe Gasparre et al. 2011) (Iommarini et al. 2014) and iii. the functional vs. structural severity these mutations induce on the activity of the complex. Consequently, mutations affecting mtDNA-encoded subunits are sub-divided in 3 groups: those mildly affecting CI function/activity, severe shifts altering the enzyme activity but not its overall stability and finally disruptive mutations which totally impair the complex assembly (Iommarini et al. 2013).

To further illustrate this concept, heteroplasmic missense or frameshift mutations in mtDNA genes encoding for CI subunits were reported to play a pro-tumorigenic role. Consistent with a mild functional alteration of the complex enzymatic activity, such mutations were shown to enhance cancer cells tumorigenic potential *in vitro* through mechanisms involving reactive oxygen species (ROS), HIF-1 α or Akt kinase signalings (Leone et al. 2018). In the same time, growing evidence is emerging to support the contribution of mitochondrial mutations in CI encoding genes in metastasis and resistance to chemotherapy (Ishikawa et al. 2008) (Girolimetti et al. 2017) (Guerra et al. 2012). By contrast, at homoplasmic loads some mutations in CI mtDNA-encoded genes correlated with a reduced tumor growth *in vitro* and *in vivo* (Park et al. 2009), while studies on indolent oncocytomas carried by our group and others unveiled the high occurrence rate of mutations affecting CI genes in this tumor subtype (Gasparre et al. 2007). Further modulation of the hetero/homoplasmy levels highlighted the *oncojanus* role of mitochondrial-encoded complex I genes in affecting tumor fate, either by impinging tumor progression or on the contrary favouring it. One good example is homoplasmic 3571insC/*MT-ND1*, defined as a disruptive or disassembling mutation as it impeaches CI assembly. A homoplasmic but not heteroplasmic load of the mutation, translated at a metabolic level with imbalanced α KG over SA ratio in favour of α KG, a feature that was similarly recapitulated by genetically CI-deprived cells (Kurelac et al., 2019). The two metabolites tightly regulating the activity of prolyl hydroxylases and HIF sensing, such a metabolic context resulted in chronic HIF-1 α destabilisation ultimately blocking tumor growth both *in vitro* and *in vivo* (Porcelli et al., 2010) (Calabrese et al., 2013) (Iommarini et al., 2014) (Kurelac et al., 2019).

Hence, this knowledge gives further insight into the double-edged implication of mitochondrial CI in tumor progression, metastasis and resistance to therapy modulated by the

oncojanus role of mtDNA-encoded genes progression. Although further investigation is warranted, evidence is also emerging in favour of an *oncojnaus* implication of CI nDNA-encoded genes (Leone et al., 2018).

In continuity with this, pharmacological targeting of the complex activity could thus constitute an appealing approach for the development of new cancer therapies. In this frame, molecules have been reported thus far. Although classical compounds (alkaloids, rotenone, ptericidin A and capsaicin) displayed strong anti-proliferative properties *in vitro*, their effect is coupled to considerable ROS generation thereby compromising their use for safety issues. Many other molecules are emerging and gaining substantial interest. Amongst these, BAY 87-2243 and AG311 were described to block CI activity leading to reduced oxygen consumption and induce cancer cell death *in vitro* and *in vivo* in glucose-deprived conditions (Bastian et al., 2017). In particular, treatment with BAY87-2243 induced ROS accumulation, reduced ATP levels which correlated with AMPK activation in melanoma cells (Ellinghaus et al., 2013) (Schockel et al., 2015). More recently, biguanides, drugs approved for the treatment of type II diabetes mellitus have gained growing attention for their ability to inhibit mitochondrial CI through a non-competitive inhibition of ubiquinone reduction (Bridges 2014). From this class, a number of studies have been dedicated to studying the anti-neoplastic effect of metformin, especially after epidemiological studies revealed the drug to have protective properties on cancer onset and to ameliorate prognosis. *in vitro* the drug was reported to display an anti-proliferative effect through a specific inhibition of CI. In this context, metformin determined a bioenergetic crisis, reduced glucose oxidation in the mitochondria and increased cancer cells dependency on glutamine reductive carboxylation (Fendt et al., 2013). Like other CI inhibitors, metformin's anti-neoplastic effect was more marked under glucose starvation conditions, suggesting that cancer cells mainly use glycolysis for survival following CI inhibition (Birsoy et al., 2014) (Andrzejewski et al., 2014). Similarly, in our cell models we confirm metformin's ability to block HIF-1 α stabilisation (unpublished data) and its capacity to alter cancer cells viability and *in vitro* clonogenic abilities. However, this effect seems to be partly independent from CI activity inhibition (off-target effect) and is more important as treatment doses increase. Remarkably, metformin, BAY87-2243 and AG311 were all able to induce HIF-1 α destabilisation in hypoxic conditions in the tested models (Wheaton et al., 2014) (Ellinghaus et al., 2013) (Schockel et al., 2015). A direct consequence of CI inhibitors effect could be a stimulated activity of prolyl hydroxylases. Indeed, it is possible that reduced oxygen consumption would

increase oxygen availability thereby stimulating prolyl hydroxylases to target HIF-1 α for degradation even in low oxygen condition (*pseudonormoxia*). On the other hand, and as previously demonstrated in our CI-deprived models, NADH accumulation following the abolition of CI-dependent NADH dehydrogenase activity induces an imbalanced NAD⁺/NADH ratio that downmodulates the activity of α KG dehydrogenase complex (α KGDHC) causing α KG levels to increase ultimately boosting PHD activity (Calabrese et al., 2013) (Iommarini et al., 2014) (Kurelac et al., 2019). Other molecules interfering with the complex activity include antidiabetic canagliflozin which was able to inhibit the proliferation of prostate and lung cancer cells, reduced glucose uptake and ATP levels leading to AMPK phosphorylation (Villani et al., 2016). Similarly, antilipemic agent fenofibrate also showed the potency to reversibly inhibit the mitochondrial complex thereby inducing cancer cells apoptotic cell death *in vitro* or autophagy as a mechanism to sustain proliferation (Brunmair et al., 2004). The list of CI inhibitors still goes on with compounds from the isoflavonoids family (ME-344) or JCI-20679 all of which were reported for their repressive potential on the complex activity and on cancer cell growth (Lim et al., 2015) (Akatsuka et al., 2016). However, before future therapeutic applications on clinical patients, the mechanism and specificity of action as well as safety of each respective candidate still need to be clearly assessed.

α KG as an anticancer agent

In light of *in vitro* affinity studies on different α KGDDs (Koivunen et al., 2007), further studies demonstrated the reversible nature of α KGDDs inhibition exerted by α KG analogues highlighting the importance of the ratio oncometabolite/ α KG in such a context. As first demonstrated by MacKenzie and colleagues, concomitant increase of α KG levels was able to overcome PHD inhibition mediated by SA and FA in an *in vitro* assay (MacKenzie et al., 2007). Likewise, 2-HG inhibition of histone demethylases, was also reversed by increasing amounts of α KG (Xu et al., 2011).

This knowledge opened new perspectives for novel therapeutic strategies, amongst which the possibility of using α KG as an anticancer agent to counteract oncogenic progression has emerged. About a decade ago, the first studies started investigating the ability of α KG to oppose to HIF signalling in cancer models, through a provoked intracellular accumulation of the metabolite via a genetic or pharmacologic modulation. In this frame, numerous studies set the tone, describing antitumorigenic effects of the ketoacid. Our group demonstrated that the

increased α KG/succinate and NADH/NAD⁺ ratio in cells lacking a functional mitochondrial complex I. Overall, this condition prevented HIF-1 α stabilisation and delayed tumor growth both *in vitro* and *in vivo* (Porcelli et al., 2010) (Calabrese et al., 2013) (Iommarini et al., 2014) (Kurelac et al., 2019). We demonstrated that α KG intracellular accumulation is able to enhance PHDs activity resulting in chronic HIF degradation even under low oxygen tension, a condition we termed *pseudonormoxia*. By contrast, other works used exogenous supplementation of free or conjugated α KG. Indeed, because the hydrophilic character of the molecule limits its membrane permeability, some groups opted for cell-permeable α KG ester analogues. Such compounds were shown to efficiently permeate through the plasma membrane thereby enhancing the metabolite intracellular levels to finally reverse PHD inhibition exerted by fumarate and succinate in SDH-deficient cells (MacKenzie et al., 2007) (Tennant et al., 2009). Similarly, treating Hep3B and LLC cancer cells models with exogenous α KG induced a dose-dependent HIF-1 α destabilisation in hypoxia (Matsumoto et al., 2006) (Matsumoto et al., 2009) and counterbalanced HIF-1 α -nuclear accumulation in SDH-mutant fibroblasts (Brière et al. 2005). Further, HIF-1 α targeting for proteasomal degradation subsequently to α KG-analogues exposure was mediated by PHD2 reactivation and independently of oxygen tension *in vitro* and *in vivo* (Tennant et al., 2009) (Tseng et al., 2018) further confirming the role of this isoform in HIF-1 α regulation. In continuity with this, α KG supplementation correlated with a dose-dependent downregulation of HIF downstream targets at transcriptional and post-transcriptional levels (Matsumoto et al., 2006) (Matsumoto et al., 2009) likely suggesting the ketocid also stimulates FIH1 activity. At the metabolic level, α KG severely reduced ATP levels, glucose consumption and lactate levels, finally leading to a PHD3-dependent apoptotic cell death (Tennant et al., 2009) (Tennant and Gottlieb, 2010). Moreover, in combination with respiratory chain complex I inhibitor BAY-87 2243, dimethyl- α KG was able to block glycolysis through an MDM2-dependent transcriptional reprogramming ultimately triggering parthanatos in cancer cells (Sica et al., 2019). In a metastatic breast cancer cell model α KG-based treatment enhanced oxidative phosphorylation, impaired cancer cell clonogenic properties *in vitro* and tumor growth *in vivo* (Tseng et al., 2018). Interestingly, Rzeski and colleagues reported an anti-proliferative effect of α KG on a set of colon adenocarcinomas cells in normoxia (Rzeski et al., 2012). The effect was mediated via a blockade in DNA synthesis followed by cell cycle arrest. These reports infer multiple implication of the metabolite in distinct signalling pathways that overall converge towards a single outcome that is reduced proliferation. Notably, following α KG-analogues structure optimisation, the ketoacid was able to permeate within complex 3D

structures and exhibited a high potency in blocking hypoxic signalling in colon cancer-derived tumor spheroids (Tennant et al., 2009) while tumor xenografts exposed to those analogues were significantly smaller in size and less dependent on glucose consumption (Tennant et al., 2009). Intriguingly, despite the block in tumor growth secondary to CI ablation, we showed that our CI-deficient models are able to recruit pro-tumorigenic M2 macrophages in what seems to constitute an adaptative mechanisms aiming to maintain tumor subsistence (Kurelac et al., 2019). Of note that α KG was previously reported to favour M2 macrophages polarisation (Liu et al., 2017), however in our case further investigations are necessary to determine if α KG accumulated secondary to CI ablation may result in M2 macrophages activation as a side-effect.

More recently, a bulk of studies rather highlighted the implication of α KG in the epigenetic regulation of gene expression by modulating histone and DNA demethylation, considering its role as a limiting substrate during TETs and KDMs catalysed reactions. In this frame, pharmacological or genetic inactivation of α -ketoglutarate dehydrogenase (α KGDH) induced an accumulation of intracellular α KG and translated with increased TET1 and TET3 enzymatic activity both *in vitro* and *in vivo*. Such an approach reversed DNA hypermethylation and reactivated miR-200 family pathway thereby blocking cell migration and EMT in breast cancer models (Atlante et al., 2016). To further emphasize the beneficial effect of the metabolite in opposing to the accumulation of repressive epigenetic markers, treatment with α KG counterbalanced succinate-mediated inhibition of TETs by increasing 5-hmC and reducing 5-mC in paraganglioma SDH-deficient cells (Letouzé et al., 2013). Moreover, in a pancreas ductal adenocarcinoma (PDAC) model, dimethyl- α KG administration reactivated TET-mediated DNA demethylation favouring tumor cell differentiation through a mechanism that recapitulates p53 anti-tumorigenic response (Morris et al., 2019), while it was shown to counteract Wnt hyperactivation in patients-derived intestinal organoid model (Tran et al., 2020). In addition to stimulating histone demethylation in breast cancer cells, dimethyl- α KG induced senescence and reversed resistance to genotoxic stress secondary to ionized radiation (Efimova et al., 2016).

AIMS

Solid tumors sustain their high growth rate through a metabolic and hypoxic adaptation mainly orchestrated by HIF-1 α , which controls the transcription of target genes implicated in glycolysis, neoangiogenesis and metastasis. At the clinical level, these tumors are associated with a higher risk of therapy resistance, relapse and poor prognosis in cancer patients even more that few molecules directly targeting hypoxia/HIF-1 α axis have been approved so far due to safety issues or limited therapeutic efficacy. We previously showed the lack of respiratory Complex I causes the accumulation of α KG associated with the destabilization of HIF-1 α that renders cancer cells unable to adapt to hypoxia, a condition we termed *pseudonormoxia*, and ultimately blocks tumor growth *in vivo*.

This project thus aims to propose a metabolic-based approach to tackle cancer cell proliferation through a provoked accumulation of exogenous α KG under hypoxia condition. We speculated that high levels of α KG would result in a boosted PHDs activity with subsequent activation of HIF-1 α protein degradation cascade. Although the ketoacid hydrophilic properties constitute a limitation to its membrane permeability, we generated ester analogues of α KG (α KGlogues), in which the metabolite is linked to such hydrophobic carriers via an ester bond allowing to optimise its physicochemical properties and thereby its delivery to the intracellular compartment due to the action of esterases. Consequently, a panel of 7 different α KG-monoesters were synthesised for the purpose of this study, each one bearing a structurally distinct carrier, and their ability to impede HIF-1 α stabilisation in low oxygen tension along with cancer cell growth was assessed. Simultaneously, the α KGlogues safety was tested on non-cancer cells counterpart. Further, the respective abundances of TCA cycle intermediates and the molecular consequences likely engendered by such a metabolic state in cancer cells were also investigated. Finally, taking this study a step further in the perspective of proposing an α KG-based adjuvant anti-neoplastic therapy we aimed at translating our main hypothesis in more complex *in vitro* and *in vivo* cancer models that mimic the main features of solid tumors. In this regard, the potency of the most promising analogues and their cytotoxicity was established in 3D-derived tumor spheroids and *in vivo* whole organism namely *Drosophila melanogaster* cancer model.

EXPERIMENTAL PROCEDURES

Chemical synthesis and stability analyses on α KGlogues

Aiming to increase the permeability of exogenous α KG through the plasma membrane and thus achieve cytoplasmic accumulation of the metabolite, α KG was conjugated to chemical carriers of different hydrophobic indexes thereby generating monoester analogues (α KGlogues). The panel of 7 α KGlogues were synthesized as following: the appropriate halo-derivative was added (1.1 eq) to a solution of α -ketoglutaric acid (10 mmol) and dicyclohexylamine (1.2 eq) in dimethyl formamide (50 mL), and the solution was heated at 50°C for 5-16h. The mixture was concentrated under reduced pressure, the residue was resuspended in dichloromethane (100 ml) then washed with 0.5 N aqueous hydrochloric acid (50 mL). The organic layer was dried (sodium sulfate), and the solvent was removed under reduced pressure. The crude products were purified by flash column chromatography (petroleum ether/acetone, in various proportions), or by crystallization from acetone, ethanol, ethyl acetate or petroleum ether. The structures of the final compounds were confirmed by means of ^1H -NMR spectra. The ^1H -NMR spectra were recorded on a Varian MR 400 MHz (ATB PFG probe) (Data not shown). Following chemical synthesis (Figure 6) and purity assessment using NMR technology, compounds were dissolved in 100% ethanol or in a 1:1 mixture of ethanol:DMSO (α KG-PP) then stored at -20°C. In their organic solvent the panel of α KGlogues displayed overall good stability levels, and only traces of degradation products were detected by thin layer chromatography (TLC) (Figure 7A) and quantitative mass spectrometric analysis revealed the esterified form of the compounds was prevalent to more than 99% (Figure 7B). Likewise, α KGlogues were stable up to 80% in tissue culture media reflecting minor basal hydrolysis and further confirming the compounds stability in aqueous solution (Figure 7C).

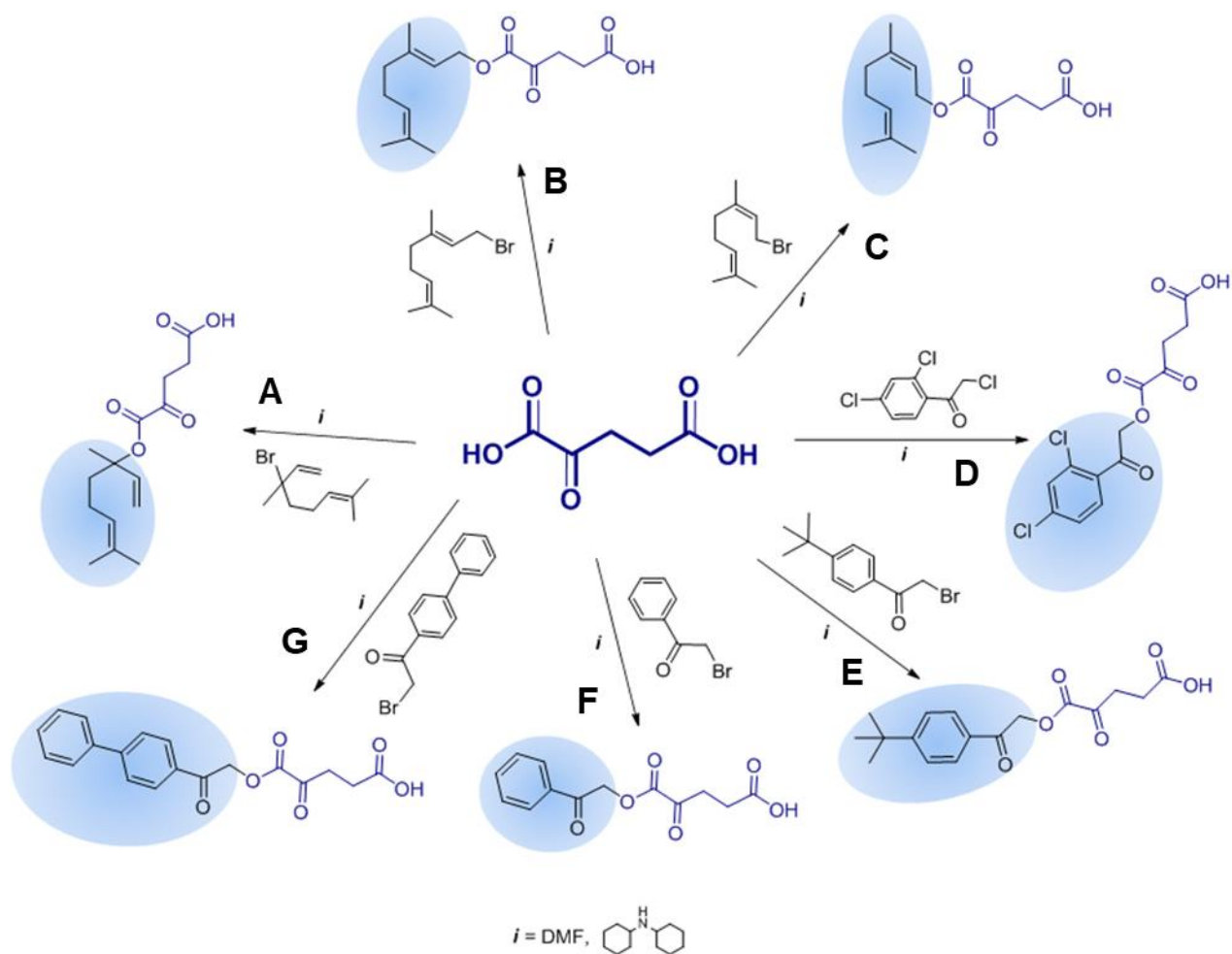


Figure 6: Schematic representation of α KGlogues chemical synthesis. Free α KG was coupled to structurally distinct hydrophobic carriers thereby giving rise to monoester analogues of α KG: α KG-L (A), α KG-G (B), α KG-N (C), α KG-Cl (D), α KG-tB (E), α KG-P (F) and α KG-PP (G) with the aim to enhance the metabolite membrane permeability.

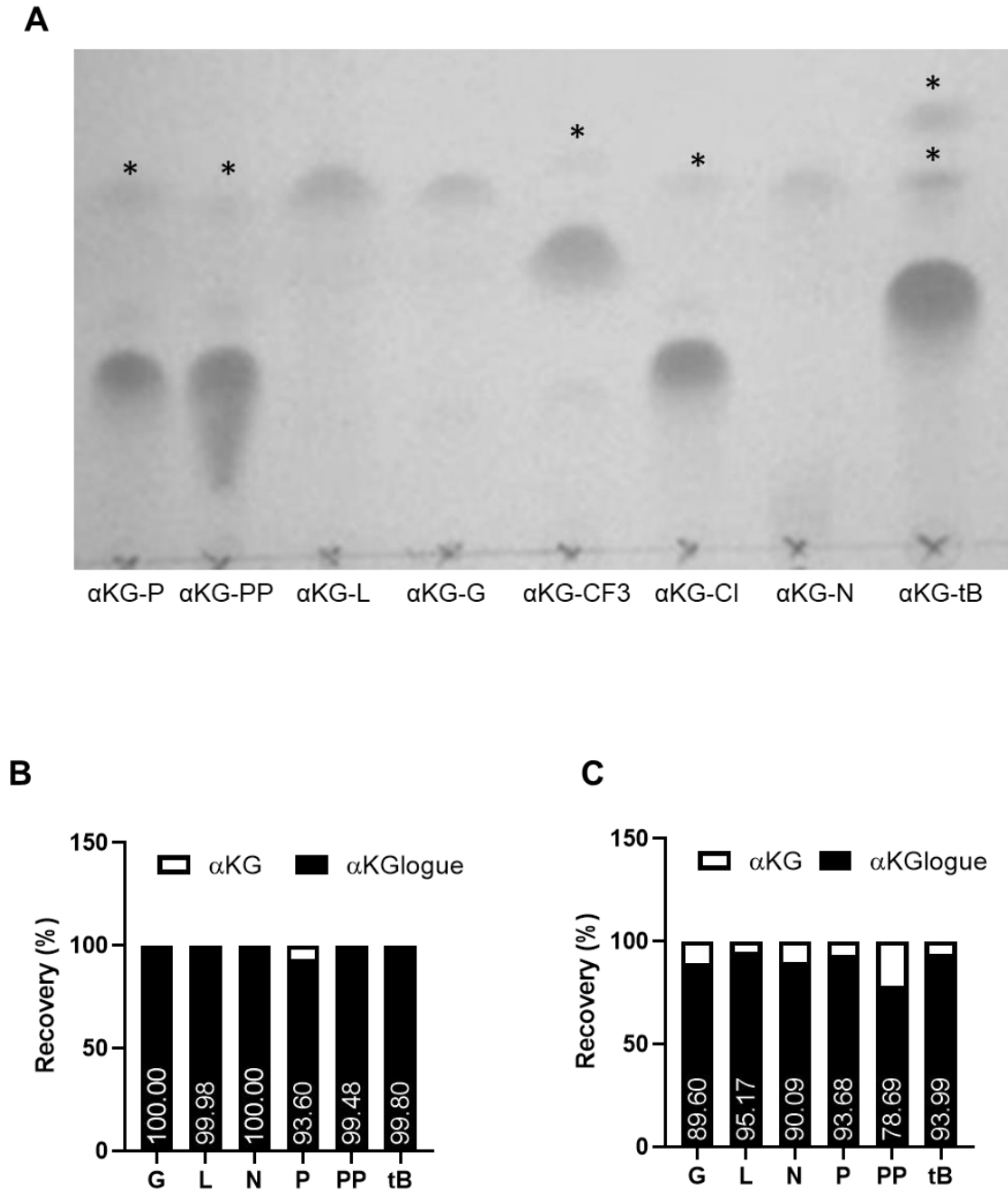


Figure 7: αKGlogues stability in organic solvent and in aqueous solution. (A) Thin layer chromatography showing mere traces of degradation of αKGlogues in organic solvent (marked with asterisks*). **(B)** αKGlogues quantitative stability data as assessed by mass spectrometric analysis respectively in organic solvent and in cell growth media unsupplemented with FBS **(C)**.

Cell culture

The cellular models used in this study, namely primary human follicular thyroid cells (N-Thy 3.1) and thyroid papillary carcinoma cells (TPC-1) were cultured in RPMI 1640 (Gibco, #21875091) while normal proximal tubule cells (HK-2) and human kidney carcinoma cells (UOK-257) of an individual with Birt-Hogg-Dubé syndrome (BHD) (Yang et al., 2008) were cultured in Dulbecco's modified Eagle medium (DMEM) high glucose media (Gibco, #21969035). Growth medias were supplemented with 10% heat-inactivated Fetal Bovine serum (FBS) (Gibco, #16000044), 100 units/mL Penicillin/100µg/mL Streptomycin (Gibco, #15140122) and 2mM L-glutamine (Gibco, #25030024). Cells were tested on a regular basis through PCR for mycoplasma detection. Where indicated, cells were exposed to 2mM of commercial α KG-DM (Sigma-Aldrich, #349631). Deferoxamine (DFO) (Novartis, #A020417022) was used at 150µM for 24h as a positive control for PHDs inhibition.

HIF-TM transduction

A non-degradable version of HIF-1 α was produced as previously described (Kurelac et al., 2019) by site directed mutagenesis of residues P402A, P564G, and N803A, HIF-targeted sites for hydroxylation by prolyl hydroxylases (PHDs) and Factor inhibiting HIF (FIH1), respectively using Quickchange Site-Directed Mutagenesis kit (Agilent, #200518). Triple-mutant HIF1A (TM-HIF) sequence was priorly transferred onto pMSCV-puro-Retroviral vector (Clontech, #PT3303-5), after which the empty vector and the vector containing HIF-TM were used to transduce TPC-1 and UOK-257 cells by following phxA transduction protocol (Takara, #631317). Cells carrying the vectors were selected with 750 ng/mL puromycin (Sigma-Aldrich, #P8833) and maintained in medium supplemented with 250 ng/mL puromycin. Clonal selection was performed to identify the clones with the highest HIF-TM protein levels in normoxia (21% O₂) and pools of at least 3 clones were made for each cell line.

SDS-PAGE & western-blotting

Where indicated and post-hypoxia exposure in presence of either 200µM unconjugated α KG, α KGlogues or PP carrier, cells were harvested and lysed in RIPA buffer (Tris-HCl 50mM pH 7.4, 1% Triton X-100, 0.1% SDS, 1mM EDTA pH 7, 150mM NaCl) supplemented with a 1X

phosphatases inhibitors (Alfa Aesar, #J63907) and 1X proteases inhibitors (Roche, #4693116001). Proteins were quantified with the Bradford method using BSA as a standard, denatured for 5 minutes at 95°C in Laemmli buffer, then loaded (30-40 µg) onto polyacrylamide gels (SDS-PAGE) and separated in a Mini-PROTEAN® Electrophoresis cell (Bio-Rad). Samples were subsequently transferred in full-wet system (Mini Trans-Blot® Cell, Bio-Rad) onto nitrocellulose membranes (Bio-Rad, #1620115), or Polyvinylidene fluoride (PVDF) (Bio-Rad, #1620177) for HIF-1α immunoblotting. Following 1h of blocking in 5% non-fat dry milk, 1X TBS (Tris Buffered Saline)-0.05% Tween® 20 (Sigma-Aldrich, #P1379), membranes were incubated overnight at +4°C with primary antibodies: anti-β-Actin (Sigma-Aldrich, #SAB5500001) 1:5000, anti-HIF-1α (GeneTex, #GTX127309) 1:2000; phospho-mTOR (S2448) (Cell Signaling Technology, #5536S) 1:1000; Phospho-Raptor (Ser792) (Cell Signaling Technology, #2083S) 1:1000; Phospho-p70S6K (S371) (Cell Signaling Technology, #9208S) 1:1000; Phospho-4E-BP1 (Thr37/46) (Cell Signaling Technology, #2855T) 1:1000. Anti-GAPDH (Sigma-Aldrich, #G8795) 1:10,000; anti-LC-3 (Sigma-Aldrich, #L7543) 1:1000; Total mTOR (Cell Signaling Technology #2983S) 1:1000; Total Raptor (Cell Signaling Technology, #2280S) 1:1000; Total p70S6K (Cell Signaling Technology, #2708S) 1:1000; were incubated for 2h at room temperature (RT). Horseradish-peroxidase-conjugated secondary antibodies (Jackson ImmunoResearch Laboratories, anti-rabbit #111-035-144, anti-mouse #115-035-146) were incubated at RT and proteins developed using Clarity™ Western ECL Substrate (Bio-Rad, #1705061). Images were acquired with Gel Logic 1500 Imaging system (Kodak, Ronchester, NY, USA). Densitometric quantification of the analysed proteins was performed using ImageJ software (NIH Image).

Cell viability

Cells were counted and plated (1×10^3 cells/well for cancer cell models and 2×10^3 cells/well for non-cancer counterparts) in 96-wells TC-treated plates (Falcon® 96 well, #353072) and left to adhere overnight. Subsequently, fresh media containing treatment (2µM, 20µM and 200µM αKGlogues or corresponding carriers) was added and cells incubated at 37°C in standard conditions (21% O₂ and 5% CO₂). Experiments carried out under low oxygen tension (1% O₂, 5% CO₂) were performed in a hypoxic workstation (Ruskin INVIVO₂ 300). Cell viability was assessed after 0, 24, 48 and 72h of treatment using sulforhodamine B

(SRB) viability assay. Briefly, at the indicated time points, cells were fixed with 50% trichloroacetic acid (TCA) (Sigma-Aldrich, #T6399), then colored with SRB (Sigma-Aldrich, #S1402) which reflects intracellular protein content (Vichai and Kirtikara 2006). SRB is an aminoxanthene dye bearing two sulfonic groups which bind to basic amino acids under mild acidic conditions and dissociate in basic conditions. Following a 30-minutes staining step and several washes in 1% acetic acid, SRB was solubilized in 10mM Tris-HCl pH 10.4 and absorbance measured at 560 nm using microplate reader VICTOR3™ (PerkinElmer, Turku, Finland). Cell viability data were expressed as percentage of cell growth with respect to time 0.

Colony forming assay (clonogenic assay)

Cells were seeded at a density of 250cell/well in 6-well plates. 24h post-seeding, treatment (200μM αKGLogues, PP carrier or vehicle) was added and cells incubated at 37°C in low oxygen tension (1% O₂, 5% CO₂, Ruskinn INVIVO₂ 300 Hypoxia workstation) for 7 days. Cells were then fixed with 50% TCA and the number of colonies counted. To evaluate protein content, colonies were stained with SRB dye after which absorbance reflecting colony size, was measured as described above.

Cell migration (wound-healing assay)

40-50 x 10³ cell/well were plated onto Incucyte® ImageLock 96-well plates (Sartorius, #4379) to reach sub-confluency. The subsequent day, a homogenous wound was realized in all wells using Incucyte® WoundMaker (Sortorius), initial media discarded, and cell monolayers washed once with Phosphate Buffer Saline (PBS) after which treatment was added. Cells were then incubated at 37°C with a fresh growth media supplemented with 1% FBS containing either vehicle or treatment (200μM αKG-tB, αKG-PP or PP carrier). Wound confluence was monitored every hour for 24h using the Incucyte® S3 Live cell Analysis System (Sartorius) in O₂ and CO₂ monitored conditions (21% O₂ and 5% CO₂).

LC-MS metabolomics analyses

For the purpose of this experiment, 5×10^5 cells were plated in 6-well plates and kept at 37°C in controlled O₂ and CO₂ conditions. 24h later, initial media was replaced, and respective treatments added, namely 200μM αKG-PP alone or in combination with 3-methyl, 2-oxovaleric acid (KMV, 2mM) (Sigma-Aldrich, #K7125), an αKG dehydrogenase complex (αKGDHC) inhibitor that was used as a positive control to induce endogenous accumulation of αKG. Consequently, 1- and 3-hours post-treatment in high oxygen tension (21% O₂), cells were counted and accordingly metabolites extracted with an appropriate volume of ice-cold extraction solution composed of 50% methanol, 30% acetonitrile, 20% ultra-pure H₂O and 5μM d8-Valine as an internal standard. Briefly, following 3 washes in PBS, extraction solution was added (1mL/million cells) and cells incubated on dry ice for 15 minutes. Cells were then scraped, collected in tubes, kept under agitation for 15 minutes at +4°C then incubated at -20°C for 1h. Finally, samples were centrifuged for 10 minutes at 16,000 rpm at +4°C and supernatants collected to be analyzed. Liquid chromatography-mass spectrometry (LC-MS) analyses were performed using an QExactive Orbitrap mass spectrometer (ThermoFisher Scientific) as previously described (Sciacovelli et al., 2016). To determine αKG intracellular concentration, standard curves were realized with commercial αKG-DM (Sigma-Aldrich, #349631) and data were normalized to mean cell volume.

Nuclear morphology assessment

30×10^3 cells were plated on glass slides (15x15mm) and left overnight, after which initial growth media was replaced with a fresh one containing vehicle, 200μM αKG-PP or PP carrier. 72h post-treatment in high oxygen tension (21% O₂), cells were fixed for 15 minutes in 4% formaldehyde, subsequently washed 3 times in PBS then incubated with DAPI (1μg/mL) for 10 minutes. Following another 3 washes in PBS, slides were mounted using a 50% glycerol solution. Nuclei morphology upon treatment was then analyzed and images captured with an epi-fluorescence microscope (Nikon 90i wide field fluorescence microscope).

Flow cytometric analysis of apoptotic cell death

24h-post seeding, cells were incubated with treatment (vehicle, 200 μ M α KG-PP or PP carrier) and kept in culture under high oxygen tension (21% O₂, 5% CO₂). 72h after treatment initiation, cells were harvested, counted, washed twice in PBS and centrifuged 5 minutes at 300 \times g. Cell pellets were then resuspended in provided binding buffer and the prepared cell suspensions co-stained with Annexin V (AV)/Propidium iodide (PI) for 20 minutes following manufacturer's instructions (Annexin V Apoptosis Kit [FITC]) (Novus, #NBP2-29373) after which flowcytometric analysis was performed using an S3 cell sorter (Bio-Rad).

β -galactosidase-associated senescence assay

8 x 10³ cells were plated onto 24-well plates and treatment (200 μ M of α KG-PP or PP carrier) added the subsequent day, after which cells were incubated at 37°C in controlled O₂ and CO₂ conditions (21% and 5%, respectively). At experiment endpoint (72h), treatment-containing media was removed, and cells washed once in PBS then fixed for 15 minutes with the provided fixative solution (Senescence Detection Kit, Abnova, #KA0899). After two washes in PBS, cells were stained overnight at 37°C with a staining solution according to manufacturer's instructions for the detection of senescence-associated β -galactosidase activity. Images were captured using a light microscope.

Multicellular cancer-derived spheroids

To generate cancer-derived spheroids, kidney and thyroid cancer cells were seeded in 96-well Ultra Low Attachment plates (Corning, #CLS3474) in a mix of appropriate tissue culture media and 2.5% (v/v) basement membrane extract (Geltrex™) (ThermoFisher, #A1413202) to mimic extracellular matrix. Cells were then centrifuged at 130 \times g for 10 minutes at RT and incubated at 37°C for 72h to allow cell aggregation and formation of homogenously sized single spheroids (Figure 8) after which α KGlogues treatment was initiated. Cytotoxicity induced by α KGlogues and positive control (200nM staurosporine) was evaluated using Promega's CytoTox-Glo™ bioluminescence assay (Promega, #G9291) according to manufacturer's instructions. In addition, 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay was used as a complementary method to determine residual live cells in 3D models. Upon treatment with α KG-PP, kidney-derived cancer spheroids were harvested

and stained with MTT dye for 4 hours at 37°C. Exceeding dye was subsequently eliminated and reduced MTT accumulated inside the cells was dissolved in DMSO. Finally, MTT absorbance reflecting metabolically active cells was measured at 560 nm using microplate reader VICTOR3™ (PerkinElmer, Turku, Finland). Spheroids size was determined using ImageJ free software (NIH).

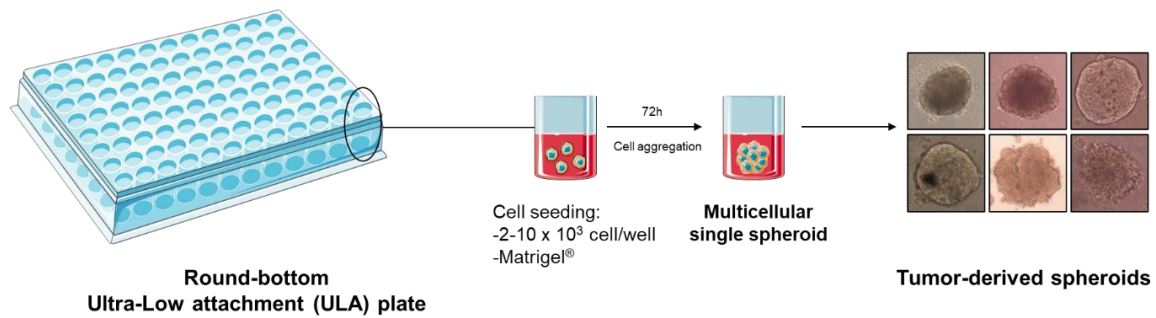


Figure 8: Generation of multicellular single spheroids as *in vitro* 3D cancer models. Cancer cells seeding in a mixture of growth media and basement membrane extract (Matrigel®) allows the formation of homogenously sized single spheroids in 96-well plates in order to test α KGlogues antiproliferative capacity. Servier Medical Art templates (<https://smart.servier.com/>) were used to generate this figure.

***Drosophila* imaginal wing discs as tumor model**

Drosophila imaginal wing discs are the larval primordium of adult fly wing. They are composed of pseudo-stratified columnar epithelium morphologically and biochemically comparable to mammalian epithelia (Wodarz and Näthke 2007) and represent a good model for proliferation studies. During larval development, the imaginal wing discs are subdivided by the anterior-posterior border (A/P) into a posterior (P) and anterior (A) compartment while the dorsal-ventral border divides the disc into a dorsal and a ventral compartment. The dorsal and ventral compartments are determined by Apterous (Ap) expression in the dorsal compartment of the organs (Butler et al., 2003).

To induce tumor growth in wing discs, UAS-Gal4 genetic system was used (Brand and Perrimon, 1993). The two components of this system are the yeast transcriptional factor Gal4 and its specific Upstream Activating Sequences (UAS). The driver line contains the Gal4 sequence under the control of a specific promoter which permits its expression in specific tissues. The responder line, instead, contains the UAS sequence upstream of a specific

transgene. The two lines are crossed, and transcription is activated in the progeny. In the used model, the contemporary *lethal giant larvae* knockdown (*lgl^{KD}*), an evolutionary preserved polarity gene, and Ras^{V12} mutation under the control of *apterous* (*ap*) promoter were induced to mimic an oncogenic cooperation mechanism. *lgl^{KD}* and Ras^{V12} expression in the dorsal compartment of the wing discs (in green in Figure 9) allows an unrestrained larval organ overgrowth and a complete altered loss of tissue architecture (Figure 9B) with respect to the wild-type counterpart (Figure 9A). The larval development of *ap-lgl^{KD}*, Ras^{V12} individuals lasts 8-9 days unlike wild-type larvae which take 5 days to complete the larval stages at 25°C. *ap-lgl^{KD}*, Ras^{V12} larvae die at pre-pupa stadium showing wing discs with tumor dorsal compartment filling the entire organs (Figure 9B). To boost the tumor phenotype the experiments was performed at 29°C.

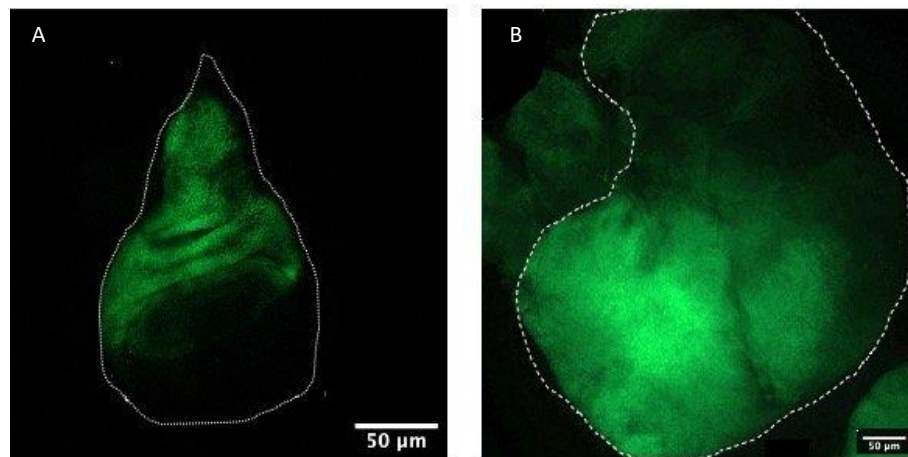


Figure 9: *Drosophila* epithelial tumor model. Wild-type (A; *ap*-GFP) and tumor (B; *ap*-GFP, *lgl^{KD}*, Ras^{V12}) imaginal wing discs. The dorsal compartments are marked in green (GFP⁺). The wing disc structures are highlighted by a dotted line. Magnification is 400X.

Fly manipulation and volume analysis

6 days after egg laying (AEL), tumor larvae were selected and divided into two groups of 25 individuals each: a control and a treated group which received vehicle and 200µM αKG-PP, respectively. 2 days after the treatment, the wing discs were isolated, photographed, and minor and major axes were measured using ImageJ free software (NIH). For volume calculation the disc shape has been approximated to a spheroid with width=depth.

Statistical analysis

GraphPad Prism 8.0 was used to perform statistical analyses and graphs generation. One-way ANOVA was performed for multiple comparison of HIF-1 α / β -Actin densitometric quantification as well as of clonogenic assay data. Two-way ANOVA was performed to analyze cell viability experiments and compounds efficacy. Finally, an unpaired t-test was performed to compare two groups unless stated otherwise. Statistical significance was considered for a p -value $p \leq 0.05$.

RESULTS

Selected α KGlogues are able to prevent HIF-1 α stabilization in hypoxia

We previously demonstrated that increased levels of intracellular α KG in respiratory complex I defective models are associated with reduced HIF-1 α stabilization in hypoxia (Kurelac et al., 2019). Thus, we hypothesize that such condition, termed *pseudonormoxia*, can be obtained through the supplementation of α KG to cells. However, because of its low hydrophobicity, α KG is poorly permeable through the plasma membrane and we pursued the strategy of conjugating the metabolite with hydrophobic substituents to improve its permeability. To investigate the ability of cell permeable α KGlogues to induce a pseudonormoxic state, HIF-1 α protein levels in hypoxia (1% O₂) were analysed in thyroid papillary carcinoma (TPC-1) and kidney carcinoma (UOK-257) cells upon incubation with 7 different α KGlogues. Commercial α KG-DM was used as a reference for compound's effectiveness. HIF-1 α levels assessed by immunoblotting, revealed that at the dose of 200 μ M, α KGlogues displayed different effects on HIF-1 α protein stabilisation in hypoxia (Figure 10) after 60 and 90 minutes of treatment. In TPC-1 cells, analogues α KG-G, α KG-N, α KG-L, α KG-tB and α KG-Cl significantly reduced HIF-1 α destabilisation after 60 and 90 minutes of incubation in hypoxia with respect to the untreated cells (Figure 10A-C). However, among these compounds only α KG-N and α KG-Cl were more effective than commercially available α KG-DM (Figure 10A-C). By contrast, α KG-P and α KG-PP showed a paradoxical effect, by increasing HIF-1 α protein levels after 90 minutes of treatment (Figure 10A-C). In UOK-257 cells, α KG-PP stood out as the most potent compound, being able to significantly reduce HIF expression after 60 minutes with respect to control and maintain this effect up to 90 minutes (Figure 10D-F). Interestingly, while the impact of 200 μ M of α KG-G and α KG-Cl was noted only after 90 minutes of treatment in hypoxia, the effect of α KG-N and α KG-P was transient, since they were effective after 60 minutes in destabilizing HIF-1 α , but the levels of the protein increased again after 90 minutes of incubation (Figure 10D-F). However, α KG-PP, α KG-G and α KG-Cl were all more effective than α KG-DM, which in turn seemed to not significantly affect on HIF-1 α levels (Figure 10D-F). We tested the effect of such compounds also in non-cancer models derived from the same tissue, namely N-Thy 3.1 for thyroid and HK-2 for kidney. Overall, α KGlogues did not impair HIF stabilisation in the healthy thyroid cells up to 90 min of exposure in hypoxia, with the exception of α KG-L and α KG-Cl which showed a transient slight reduction of HIF-1 α abundance at 60 minutes (Figure 11A-C). Similarly, in the healthy kidney counterpart, most compounds had no effect on HIF-1 α destabilisation for the duration of treatment, with the only remarkable exception of 60

minutes of exposure to α KG-PP that induced a transient reduction in HIF-1 α levels (Figure 11D-F).

Hence, from the first phase of screening, the most potent compounds limiting HIF-1 α accumulation in hypoxia were selected for further investigation, namely α KG-N, α KG-L, α KG-Cl and α KG-tB on thyroid cancer cells and α KG-G, α KG-N, α KG-Cl, α KG-P and α KG-PP on the kidney cancer cells.

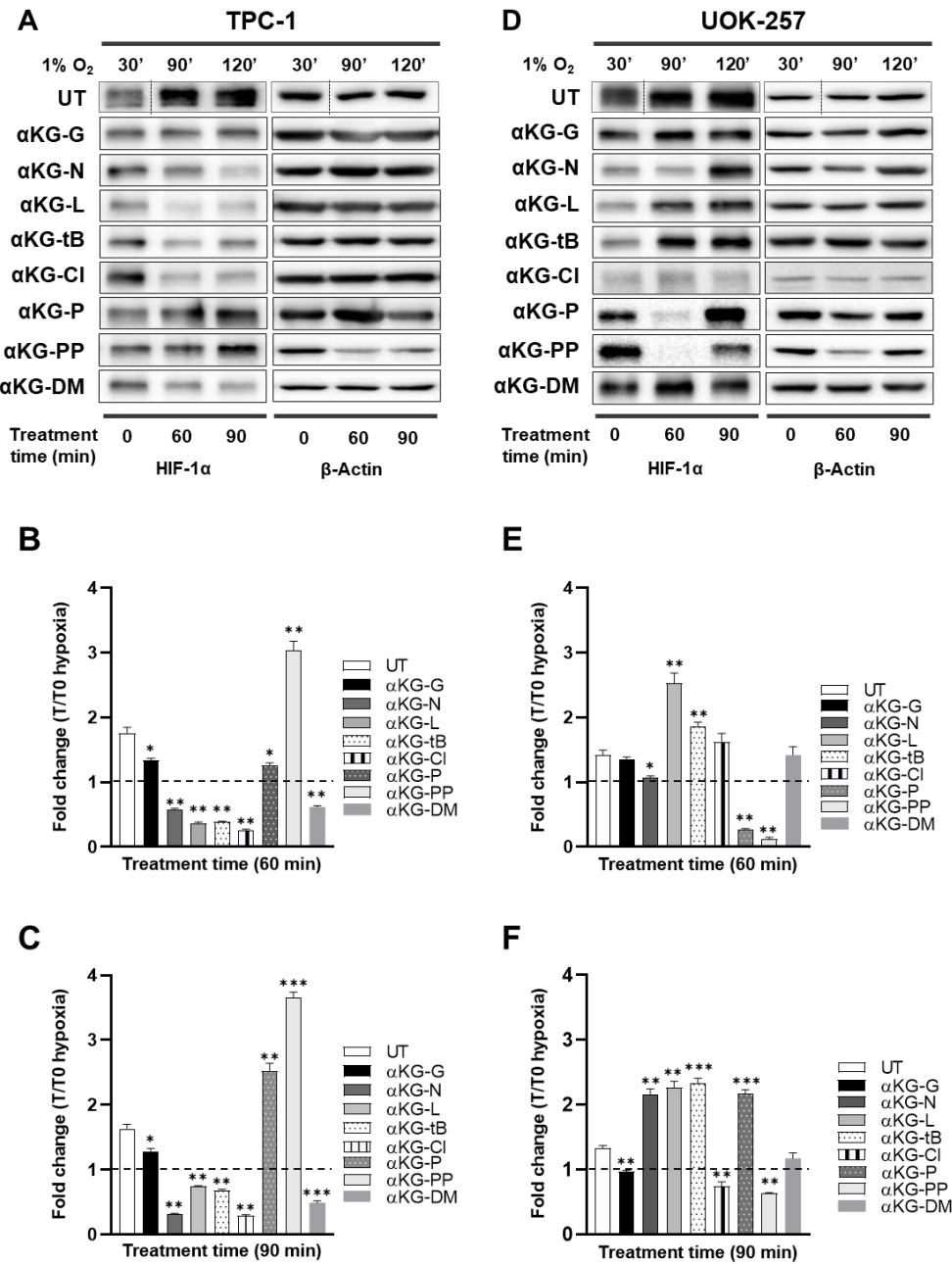


Figure 10: HIF-1α expression in cancer cell models treated with αKGlogues panel under low oxygen tension reveals promising compounds. Western blot and related densitometric analysis of HIF-1α levels in TPC-1 (A-C) and UOK-257 (D-F) cells at 60- and 90-minutes post-treatment with 200μM αKGlogues in hypoxia (1% O₂). β-Actin was used as a loading control. Data (mean ± SD) are expressed as HIF-1α/β-Actin ratio calculated at treatment time (T) and normalised on their respective untreated counterpart at T0 (30 minutes of hypoxia baseline) (n=3). A one-way ANOVA was performed for statical analysis. * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$

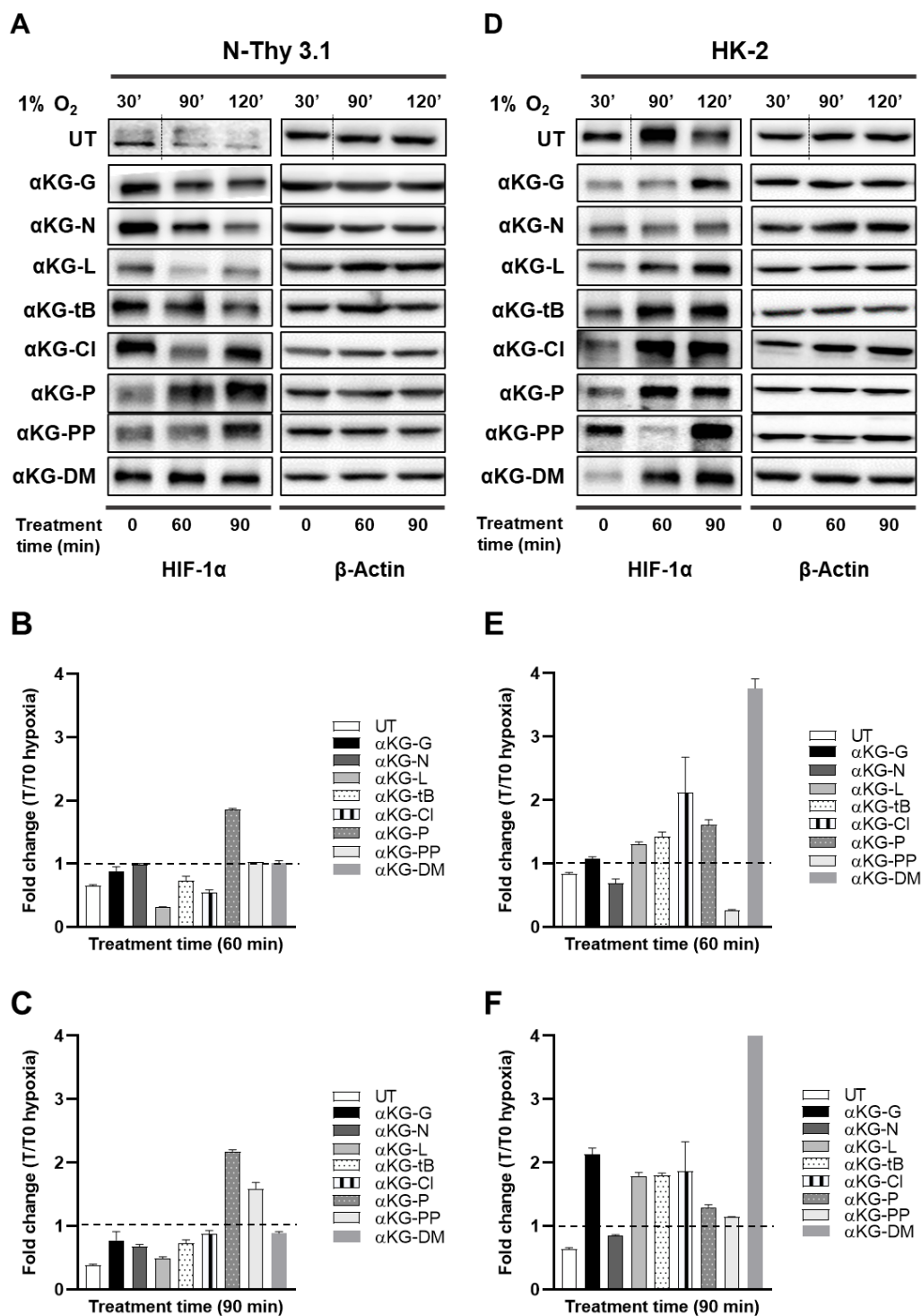


Figure 11: HIF-1α levels in non-cancer epithelial cells are not influenced by treatment with αKGlogues. Western blot and related densitometric analysis of HIF-1α levels in N-Thy 3.1 (A-C) and HK-2 (D-F) cells at 60- and 90-minutes post-treatment with 200μM αKGlogues in hypoxia (1% O₂). β-Actin was used as a loading control. Data (mean ± SD) are expressed as HIF-1 α/β-Actin ratio calculated at treatment time (T) and normalised on their respective untreated counterpart at T0 (30 minutes of hypoxia baseline) (n=2).

α KGlogues specifically alter cancer cells growth and *in vitro* tumorigenic properties

After establishing α KGlogues block HIF-1 α stabilisation in hypoxia at a dose of 200 μ M in our cancer cell models, the most effective compounds selected were then tested for their ability to alter cancer cell growth *in vitro*. Hence, in the presence of increasing concentrations of compounds, the growth of thyroid and renal cancer cells was determined along with their non-cancer counterparts, namely TPC-1/N-Thy 3.1 and UOK-257/HK-2, respectively. Cell viability following treatment was evaluated after 24, 48 and 72h of incubation using the SRB assay both in hypoxia (1% O₂) and normoxia (21% O₂). Despite the significant reduction of HIF-1 α levels in hypoxic conditions, α KG-N did not affect the growth of TPC-1 cells after 72h neither in hypoxia nor in normoxia even at the highest dose (200 μ M) (Figure 12A-B). Likewise, α KG-L was ineffective at lower doses both in hypoxia and normoxia, even if at 200 μ M the analogue slightly delayed the growth of TPC-1 cells after 3 days in hypoxia (Figure 12C-D). These two compounds resulted ineffective in the non-cancer counterpart N-Thy 3.1 (Figure 13A-D). Conversely, α KG-Cl induced a dose- and time-dependent restriction of TPC-1 cell growth (Figure 12E-F). In particular, 200 μ M of α KG-Cl was able to completely block the growth of TPC-1 cells already after 24h of treatment both under hypoxic (1% O₂) and normoxic conditions (21% O₂), while at lower doses this compound resulted more effective in hypoxia. Similarly, 20 μ M α KG-Cl displayed an early severe effect after 24 and 48 hours of incubation of N-Thy 3.1 cells, while high doses of the compound drastically altered their proliferation (Figure 13E-F). Low doses (2 and 20 μ M) of α KG-tB provoked a mild reduction of TPC-1 cell growth after 72h in low and high oxygen tension, while high doses (200 μ M) displayed a strong alteration on cells growth already after 24h of treatment independently of oxygen level (Figure 12G-H). Conversely, N-Thy 3.1 cells were not affected by low doses of α KG-tB, and only 200 μ M of the analogue correlated with a mild growth reduction independently of oxygen conditions as cells maintained their proliferation (Figure 13G-H). To discriminate the effect of the compounds on cancer vs non-cancer cells, compounds efficacy at 72h representing the percentage of dead cells induced by 200 μ M of treatment was calculated with respect to the untreated control in both cancer and non-cancer cells (Figure 14A-B). This analysis identified α KG-tB as the only compound able to selectively target TPC-1 cells without being deleterious for N-Thy 3.1 cells, as highlighted by a calculated efficacy of 80% in favour of the TPC-1 over N-Thy 3.1 (50%) (Figure 14A-B).

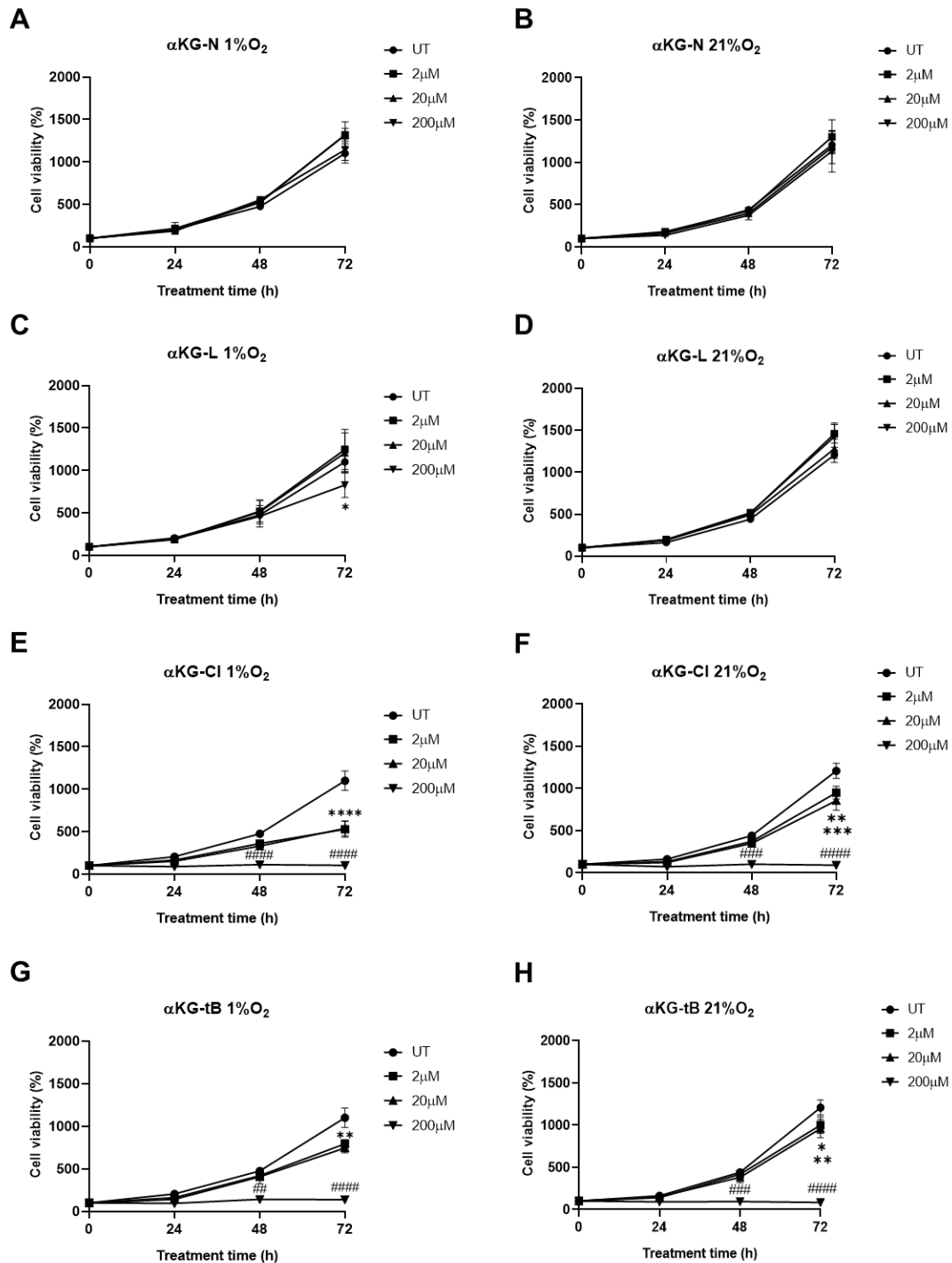


Figure 12: High doses of α KG-Cl and α KG-tB significantly alter the growth of papillary thyroid carcinoma cells despite of oxygen level. TPC-1 cell viability was determined by using SRB assay up to 72h of treatment with different doses of α KG-N (A, B), α KG-L (C, D), α KG-Cl (E, F), α KG-tB (G, H) respectively in hypoxia (1% O₂) and normoxia (21% O₂). Data (mean \pm SE) are expressed as a percentage of cell growth with respect to time 0 considered as 100% (n \geq 3). *p*-value was calculated with a two-way ANOVA. **p* \leq 0.05, ***p* \leq 0.01, ****p* \leq 0.001, *****p* \leq 0.0001

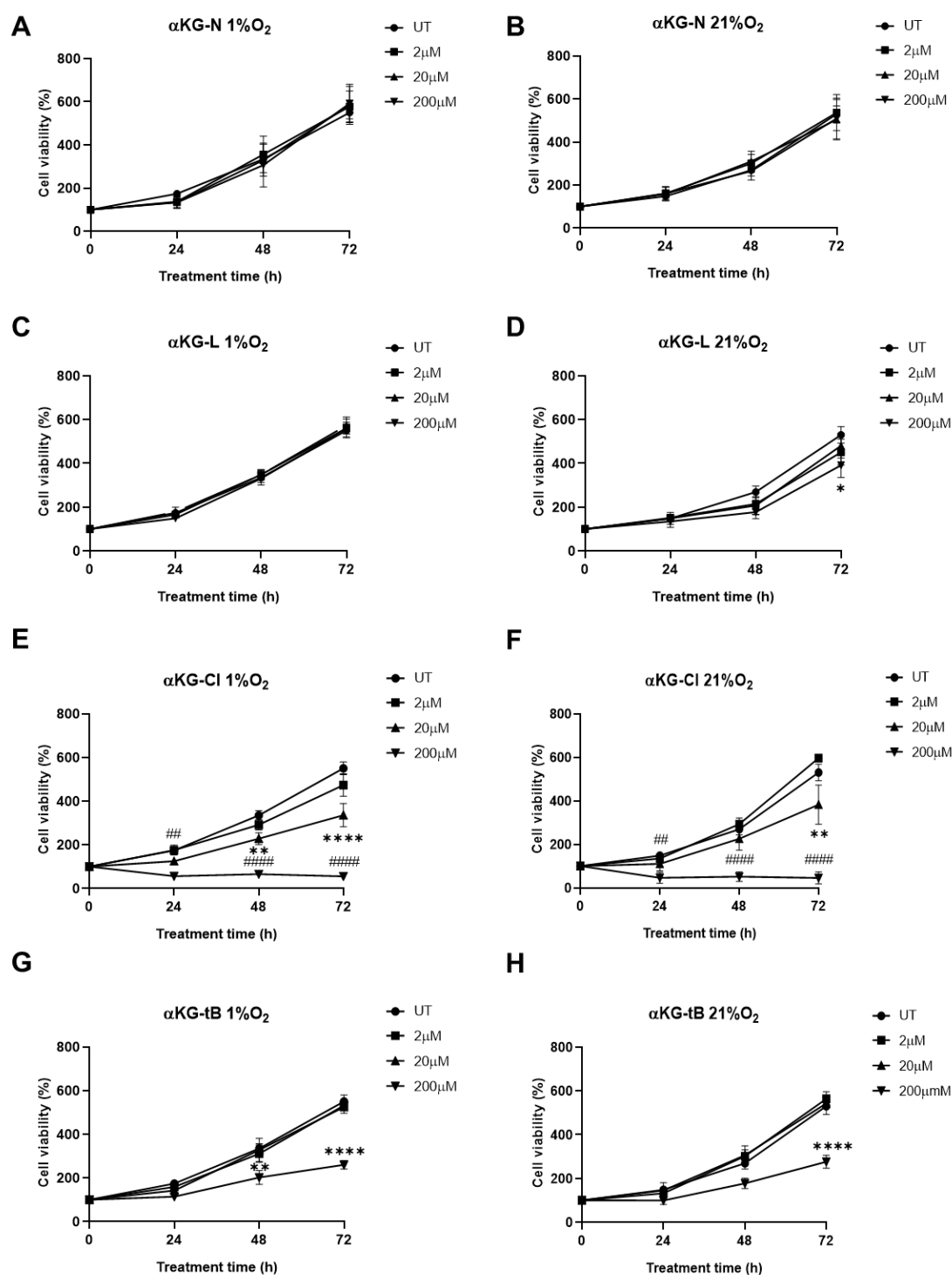


Figure 13: Proliferation of non-cancer thyroid cells is severely impaired by high doses of αKG-Cl. N-Thy 3.1 growth rate was determined by using SRB assay up to 72h of treatment with increasing doses of αKG-N (A, B), αKG-L (C, D), αKG-Cl (E, F), αKG-tB (G, H) respectively in hypoxia (1% O₂) and normoxia (21% O₂). Data (mean ± SE) are expressed as a percentage of viable cells with respect to time 0 considered as 100% (n≥3). *p*-value was calculated with a two-way ANOVA. **p*≤0.05, ***p*≤0.01, ****p*≤0.001, *****p*≤0.0001

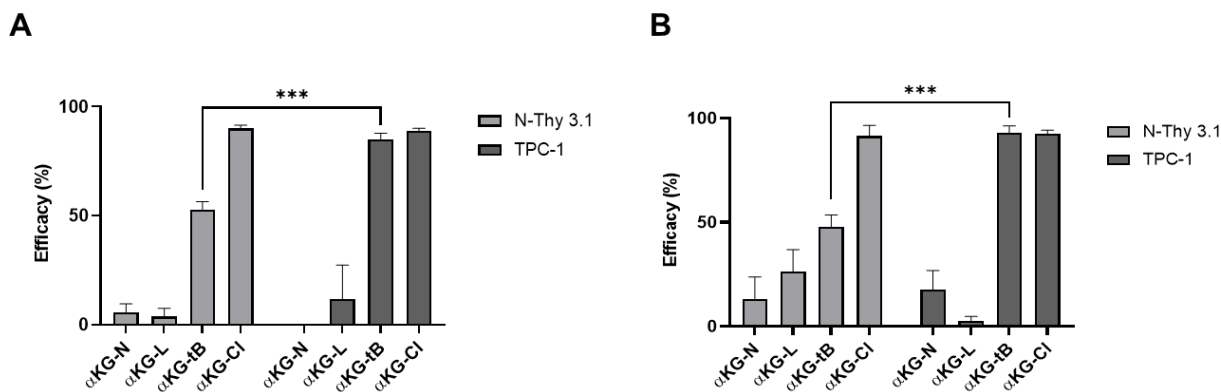


Figure 14: α KGtB selectively alters the proliferation of papillary thyroid carcinoma cells. (A-B) Efficacy of selected α KGlogues was determined in thyroid cancer (TPC-1) and non-cancer (N-Thy 3.1) cells under low (1% O₂) (A) and high oxygen tension (21% O₂) (B), respectively. Data (mean \pm SEM) represent the percentage of dead cells induced by 200 μ M α KGlogues at 72h calculated with respect to the untreated control for each cell line ($n \geq 3$). A two-way ANOVA was used to calculate p -value. * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$

With regards to the growth curves of the UOK-257 cells, the kidney carcinoma cells were insensitive to increasing doses of α KG-N, α KG-G and α KG-P up to 200 μ M either in hypoxia (1% O₂) or normoxia (21% O₂) (Figure 15A-D, G-H) and the three compounds resulted equally non-effective on the proliferation of the epithelial kidney counterparts (Figure 16A-D, G-H). By contrast, α KG-Cl induced a mild yet significant alteration in the growth of UOK-257 cells at low doses (2 and 20 μ M) 48 and 72h after treatment initiation in hypoxia, while a dose of 200 μ M caused a severe block in the proliferation of the kidney carcinoma cells during the first 2 days of the treatment in hypoxia to finally induce cell death, an effect that was observed already 24h post-treatment in normoxia (Figure 15E-F). Similarly to α KG-Cl, 2 and 20 μ M of α KGlogue-PP significantly delayed the proliferation of the UOK-257 cells at day 3 of treatment both in high and low oxygen tension whilst 200 μ M of compound blocked the growth of the cancer cells and ultimately resulted in a lethal effect at 72h (Figure 15I-J). With regards to the effect of α KG-Cl and α KG-PP on the non-cancer kidney counterpart, HK-2 cells displayed a slightly slowed growth rate after 72h of exposure to low doses of the analogues in hypoxia, and although cells suffered a drop in proliferation with 200 μ M of α KG-Cl in hypoxic as well as in normoxic conditions (Figure 16E-F), the effect remained relatively harmless as reflected by compound's efficacy (Figure 17A-B). Most importantly, α KG-PP affected the non-cancer renal cells viability to a lesser extent. In fact, it

shows to be more specific on the UOK-257 cells (80%) than on the non-cancer control (50%) in low oxygen levels (Figure 17A-B). Overall, 200 μ M of α KG-Cl and α KG-PP specifically impaired the growth of the kidney carcinoma cells while displaying safety on the epithelial counterpart (80% vs. 50% of efficacy rate for α KG-Cl and 90% vs. 70% for α KG-PP) (Figure 17A-B).

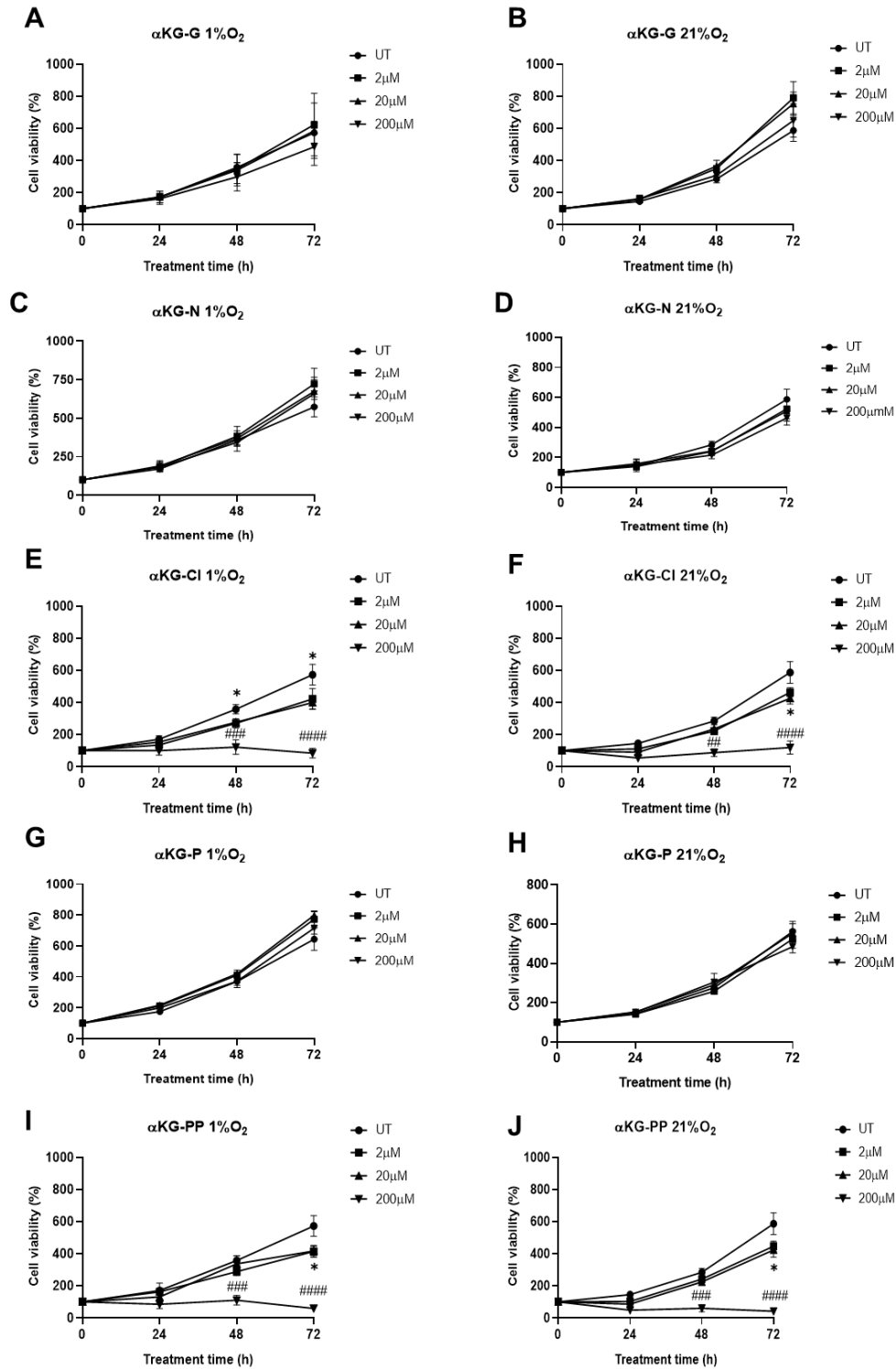


Figure 15: High doses of $\alpha\text{KG-Cl}$ and $\alpha\text{KG-PP}$ block the growth of kidney carcinoma cells indifferently from oxygen tension. UOK-257 cell viability was determined using SRB assay up to 72h of treatment with growing concentrations of $\alpha\text{KGlogues}$: $\alpha\text{KG-G}$ (A, B), $\alpha\text{KG-N}$ (C, D), $\alpha\text{KG-Cl}$ (E, F), $\alpha\text{KG-P}$ (G, H) and $\alpha\text{KG-PP}$ (I, J) respectively in hypoxia (1% O_2) and normoxia (21% O_2). Data (mean \pm SE) are expressed as a percentage of viable cells with respect to time 0 considered as 100% ($n \geq 3$). p -value was calculated using a two-way ANOVA. * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$, **** $p \leq 0.0001$

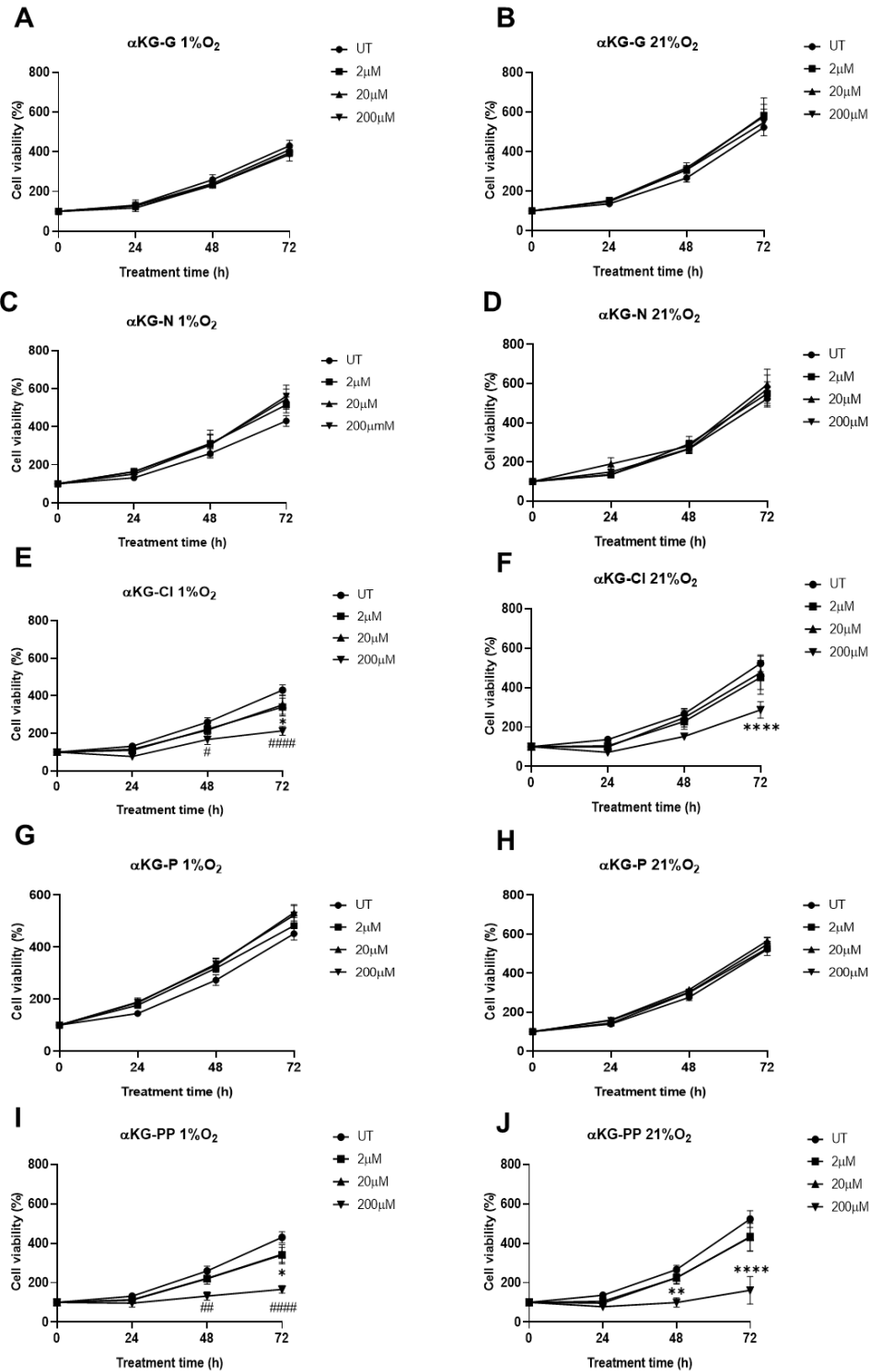


Figure 16: High doses of $\alpha\text{KG-Cl}$ and $\alpha\text{KG-PP}$ mildly delay the growth of epithelial kidney cells. HK-2 growth rate was determined using SRB assay up to 72h of treatment with increasing doses of αKG logues: $\alpha\text{KG-G}$ (A, B), $\alpha\text{KG-N}$ (C, D), $\alpha\text{KG-Cl}$ (E, F), $\alpha\text{KG-P}$ (G, H) and $\alpha\text{KG-PP}$ (I, J) respectively in hypoxia (1% O_2) and normoxia (21% O_2). Data (mean \pm SE) are expressed as a percentage of viable cells with respect to time 0 considered as 100% ($n \geq 3$). p -value was calculated with a two-way ANOVA. * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$, **** $p \leq 0.0001$

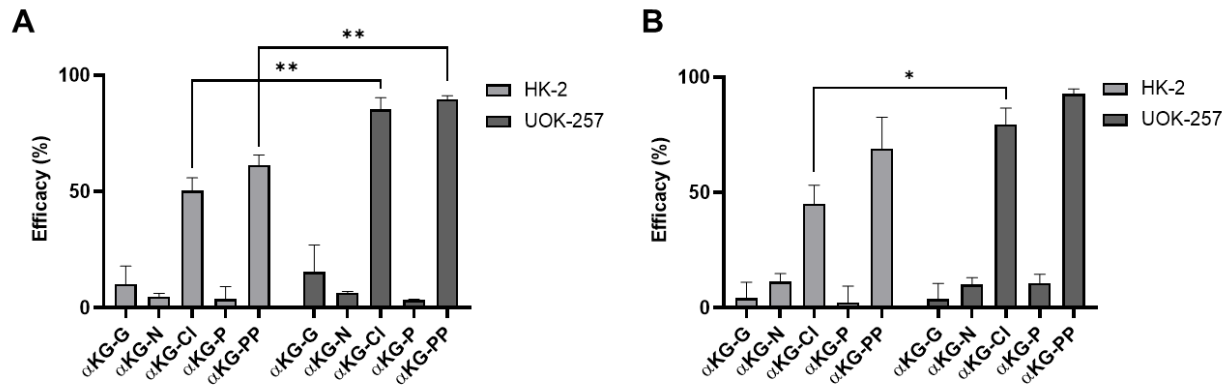


Figure 17: α KG-Cl and α KG-PP selectively impair the proliferation of kidney carcinoma cells in hypoxia. (A-B) Efficacy of selected α KGlogues was determined in kidney cancer (UOK-257) and non-cancer (HK-2) cells under low (1% O₂) (A) and high oxygen tension (21% O₂) (B), respectively. Data (mean \pm SEM) represent the percentage of dead cells induced by 200 μ M α KGlogues at 72h calculated with respect to the untreated control ($n \geq 3$). A two-way ANOVA was used to calculate p -value. * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$

To correlate the effect of α KGlogues on cell viability with HIF-1 α stabilization, we evaluated the levels of HIF-1 α in hypoxia upon treatment with the most effective compounds for long incubation times (6h and 12h). α KG-Cl and α KG-tB were chosen for TPC-1 cells, while α KG-Cl and α KG-PP were selected for UOK-257 cells. In TPC-1 cells, HIF-1 α expression was mildly reduced in presence of α KG-Cl at 6h but recovered after 12 hours (Figure 18A, 18C), while α KG-tB sustained HIF-1 α degradation up to 12h as the protein levels were two-fold lower with respect to untreated cells (Figure 18B-C). Similarly, in UOK-257 cells α KG-Cl significantly reduced the protein abundance after 12h of treatment while α KG-PP was as potent at 6 and 12h of exposure reducing HIF-1 α levels to their half with respect to the untreated (Figure 18E-F). Interestingly, at these time points unconjugated α KG was unable to affect the hypoxic HIF-1 α protein stabilisation in both TPC-1 and UOK-257 cells, confirming its low cell permeability (Figure 18B-C, 18E-F).

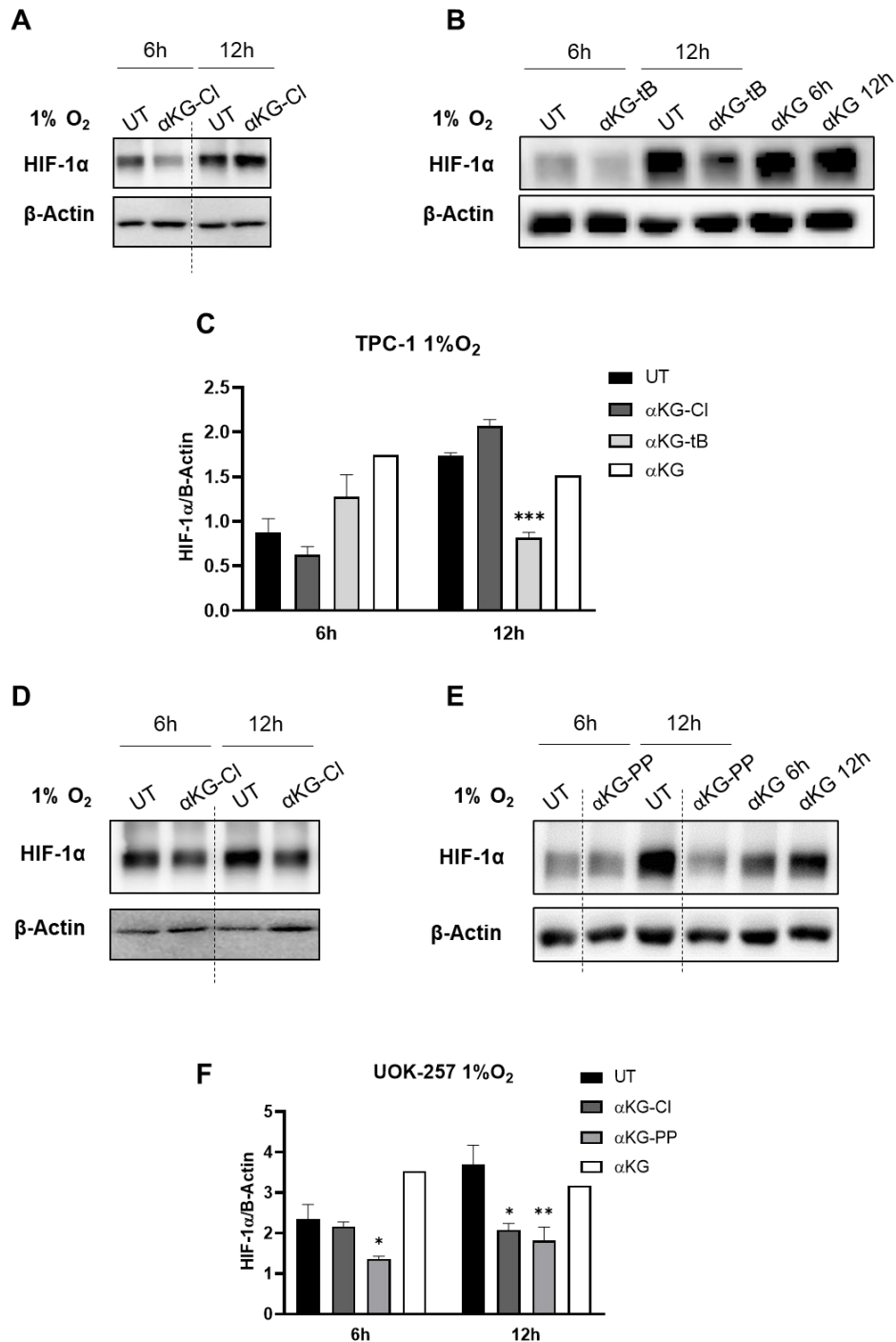


Figure 18: Selected α KGlogues sustain HIF-1 α destabilization in low oxygen tension. Western blot analysis of HIF-1 α expression in TPC-1 cells exposed to 200 μ M α KG-Cl (A), α KG-tB and unesterified α KG (B). Western blot analysis of HIF-1 α expression in UOK-257 cells treated with 200 μ M α KG-Cl (D), α KG-PP or unconjugated α KG (E) for 6 and 12 hours. Densitometric quantification of HIF-1 α protein levels both in TPC-1 (C) and UOK-257 (F) cells was performed using ImageJ software and normalised to loading control β -actin. Results (mean \pm SEM) are representative of at least 2 experiments. A two-way ANOVA was performed for statistical analysis. * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$

To test the ability of our selected hits to alter malignant cells tumorigenic properties *in vitro*, TPC-1 and UOK-257 cells were incubated in low oxygen conditions (1% O₂) with 200µM of selected αKGlogues. To this aim, we performed a colony formation assay in hypoxia to assess clonogenic properties and a wound-healing assay to determine cell migration upon treatment with selected compounds. In colony formation assay, cells were incubated for 7 days with αKGlogues and colonies were stained with SRB in order to determine the colony number and the quantification of protein content as an indicator of colony size. In these experiments, αKG-CI was not investigated since we identify an intrinsic detrimental effect on the healthy thyroid cells even at low doses, thereby only leaving αKG-tB and αKG-PP as the most promising compounds on the TPC-1 and UOK-257, respectively. In line with the viability data, 200µM αKG-tB drastically reduced the number and the size of colonies of TPC-1 cells (Figure 19A). The same parameters were severely affected by the treatment of UOK-257 cells with 200µM αKG-PP (Figure 19B). These results suggest that the analogues able to induce HIF-1α degradation in hypoxia up to 12h and to block cell growth are also able to impinge the clonogenic ability of cancer cells. Then, we analysed cancer cell mobility in a wound-healing assay. Cells were seeded in order to reach confluence after 24h, when wound was produced followed by incubation with 200µM of selected compounds. The analysis of wound confluence after 24h from the wounding event revealed that TPC-1 cells treated with 200µM αKG-tB showed a wound confluence of about 40% while untreated cells were almost able to close the wound with a confluence of 70% (Figure 19C). Similarly, after 24h the wound surface in untreated UOK-257 was at 45% confluence, while UOK-257 treated with 200µM αKG-PP showed a wound with a confluence of 15% (Figure 19D) highlighting the effectiveness of the two αKGlogues in limiting cancer cells migration ability *in vitro*.

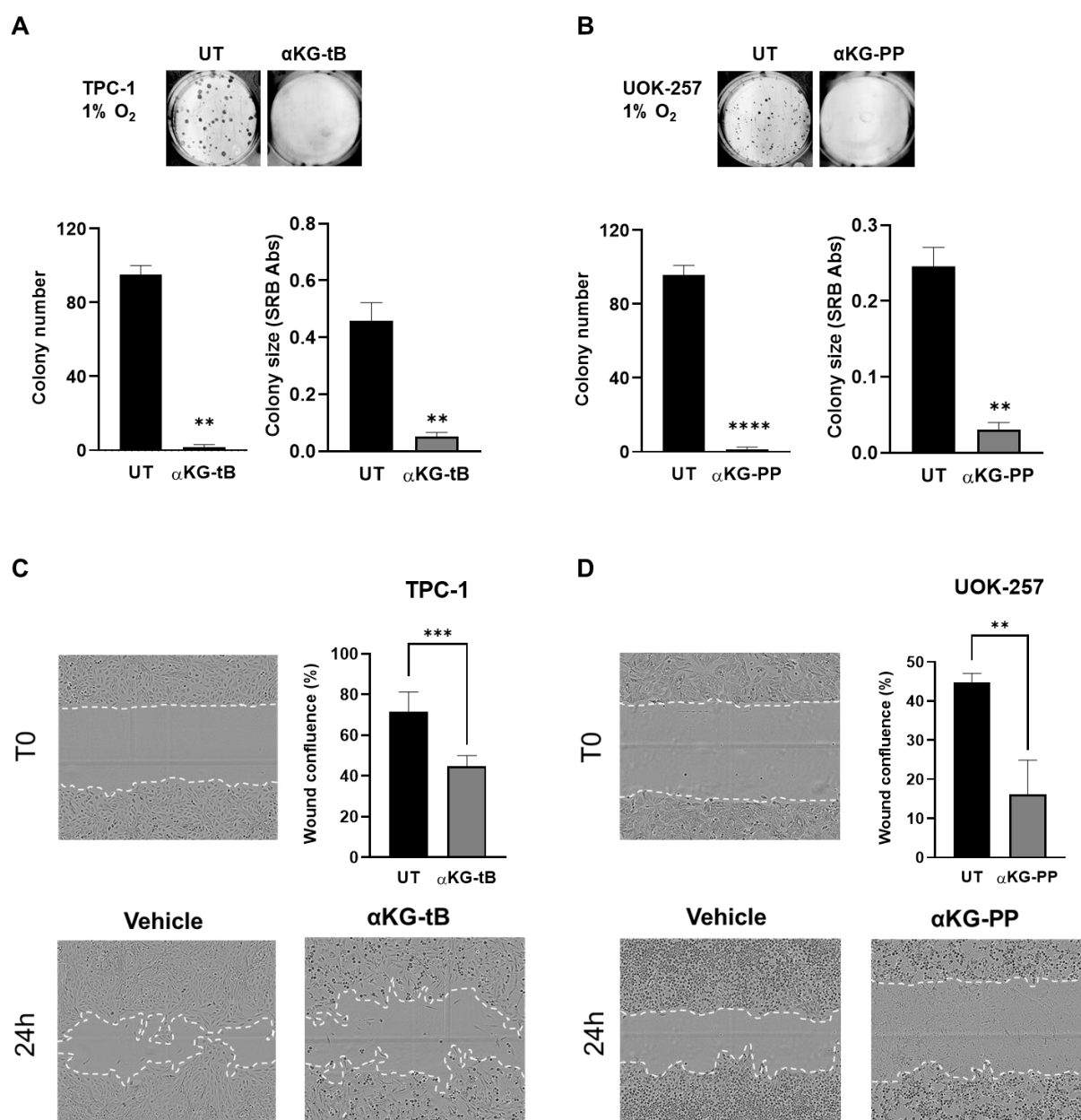


Figure 19: αKGlogues severely hamper tumorigenic properties of thyroid and kidney cancer cells *in vitro*. (A, B) Clonogenic assay was performed on untreated (UT) and treated TPC-1 and UOK-257 cells after incubation with 200μM αKG-tB or αKG-PP respectively, for 7 days in low oxygen conditions (1% O₂). Colony number was counted, and colony size determined by SRB dye absorbance measured at 560 nm. An unpaired t-test was performed for statistical analysis of data (mean ± SEM) (n=3) * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$, **** $p \leq 0.0001$. (C, D) Cell migration was evaluated through a wound-healing assay in presence of the most promising analogues: αKG-tB in TPC1 and αKG-PP in UOK-257 under high oxygen tension (21% O₂). Wound making was realised on cell monolayers at time 0 (T0) and wound closure monitored for 24h using Incucyte® S3 Live cell Analysis System. Wound confluence in TPC-1 (C) and UOK-257 (D) monolayers was calculated at experiment endpoint using Incucyte® S3 Live cell Analysis System Software. An unpaired t-test was used for statistical analysis of data (mean ± SEM) (n=3) * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$

Long-term effect on cancer cell viability is partially related to HIF pathway alteration

Selected α KGlogues, namely α KG-PP and α KG-tB, induced HIF-1 α degradation in hypoxia, which correlated with impaired cell proliferation and repressed tumorigenic properties. In order to investigate whether such alterations are caused by the shut-off of HIF-1 α signalling the two cell models were transduced to stably express a triple-mutant non-degradable version of HIF-1 α (HIF-TM). After showing the cells successfully stabilise HIF-1 α in high oxygen levels (Figure 20A, 20E), their proliferation rate was subsequently determined in presence of the selected compounds and the respective hydrophobic carriers (Figure 20B-C, 20F-G). Surprisingly, TPC-1 cells expressing HIF-TM were as sensitive to α KG-tB as to tB hydrophobic carrier (Figure 20B-D). Indeed, 200 μ M of both treatments blocked the growth of the transduced cell line, leaving only 10% viable cells after 72h and thus suggesting a non-specific effect of the carrier. Moreover, parental TPC-1 cells displayed a similar growth alteration in response to treatment with 200 μ M α KG-tB or the corresponding hydrophobic carrier (Figure 20B-D). These data suggest that the anti-proliferative effect observed with α KG-tB is independent of HIF-1 α destabilisation and solely due to the activity of the carrier, and thus not related to increased intracellular levels of α KG. By contrast, in the parental UOK-257 the residual viability in response to treatment with 200 μ M α KG-PP was of 10% viable cells, while the counterpart expressing HIF-TM is less affected by the compound with a 60% residual viable cells after 72h (Figure 20F, 20H). Interestingly, PP carrier alone similarly reduced to 60% the viability in both parental and HIF-TM expressing cells, thereby suggesting this molecule alters kidney cancer cell proliferation independently of HIF-1 α status by 40% (Figure 20F-H). Hence, PP carrier appears to contribute in part to the reduced cell proliferation and displays an additive effect to that of α KG. In light of these results, α KG-tB was therefore excluded from the study thus leaving only α KG-PP as a selected hit.

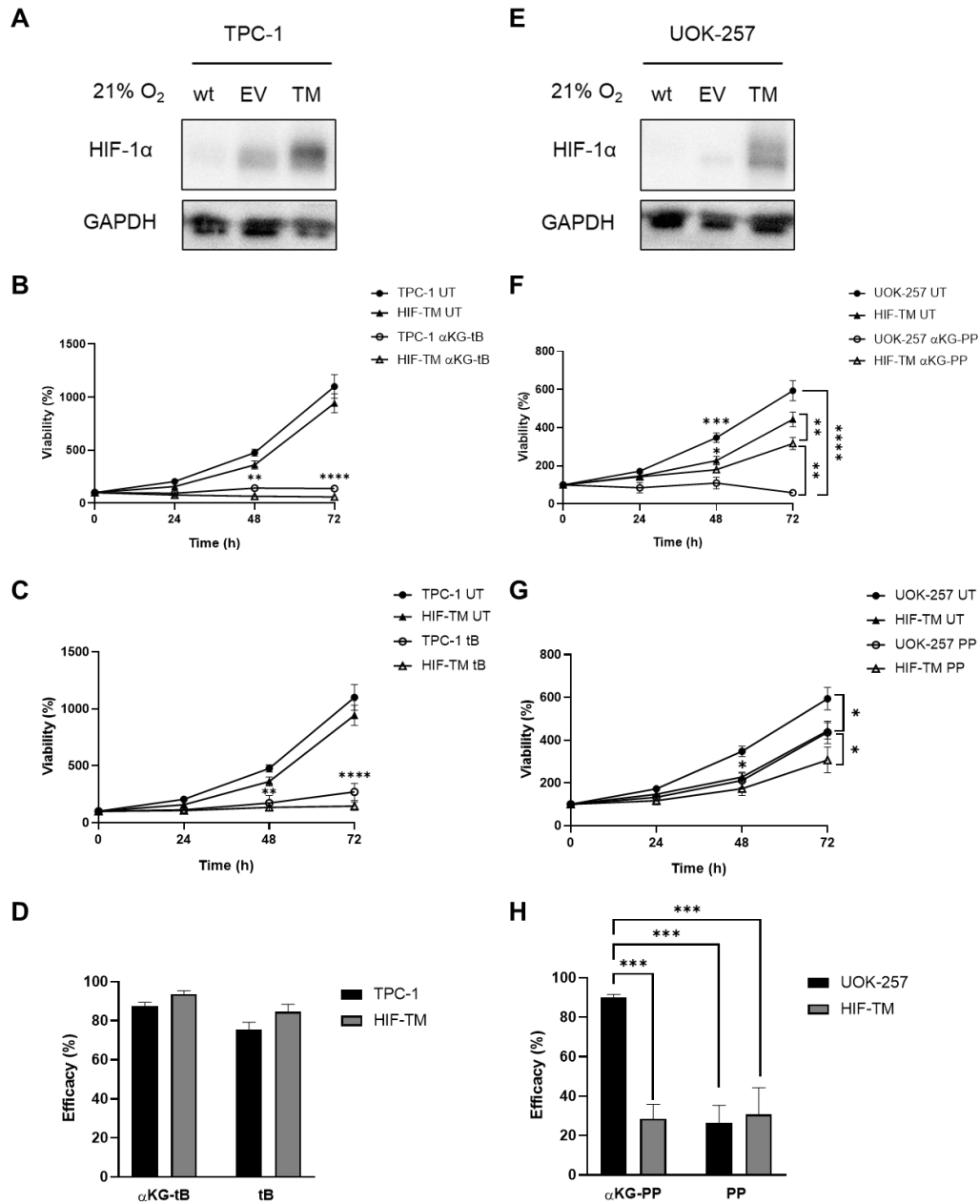


Figure 20: Hydrophobic carriers contribute to the alteration of cancer cell growth independently of HIF-1α signalling. Growth curves of TPC-1 (**A**) and UOK-257 (**E**) cells transduced with non-degradable HIF-1α (HIF-TM) in presence of 200μM αKG-tB and tB carrier (**B**, **C**) or αKG-PP and PP carrier (**F**-**G**) in normoxia (21% O₂). Curves are plotted along with the corresponding parental cell lines expressing wild-type HIF-1α exposed to the same treatments in hypoxia (1% O₂). A two-way ANOVA was used for statistical analysis of data (mean ± SEM) (n≥3) **p*≤0.05, ***p*≤0.01, ****p*≤0.001, *****p*≤0.0001, ******p*≤0.00001. Efficacy of treatment with 200μM αKG-tB and αKG-PP along with their respective carriers on TPC-1 (**D**) and UOK-257 (**H**) cell lines. Data (mean ± SEM) represent the percentage of dead cells induced by treatment at 72h calculated with respect to the untreated control in transduced and parental cell lines (n≥3). A two-way ANOVA was used for statistical analysis **p*≤0.05, ***p*≤0.01, ****p*≤0.001, *****p*≤0.0001, ******p*≤0.00001

The evaluation of colony formation and cell migration of UOK-257 cells treated with 200 μ M PP carrier confirmed its synergistic anti-proliferative activity. Indeed, UOK-257 cells treated with 200 μ M PP carrier showed an impairment in their clonogenic properties, which is however significantly lower compared with α KG-PP treatment (Figure 21A). Similarly, cell migration was impaired in cells treated with 200 μ M PP carrier, but not as much as those incubated with α KG-PP (wound confluence 30% and 15%, respectively) (Figure 21B), thereby suggesting an additive effect in this property as well. Lastly, the PP carrier alone resulted mostly well tolerated by epithelial non-cancer cells HK-2 and N-Thy 3.1 cells which were respectively viable to 70% and 50% after 72h of treatment with 200 μ M of carrier (Figure 21C-D).

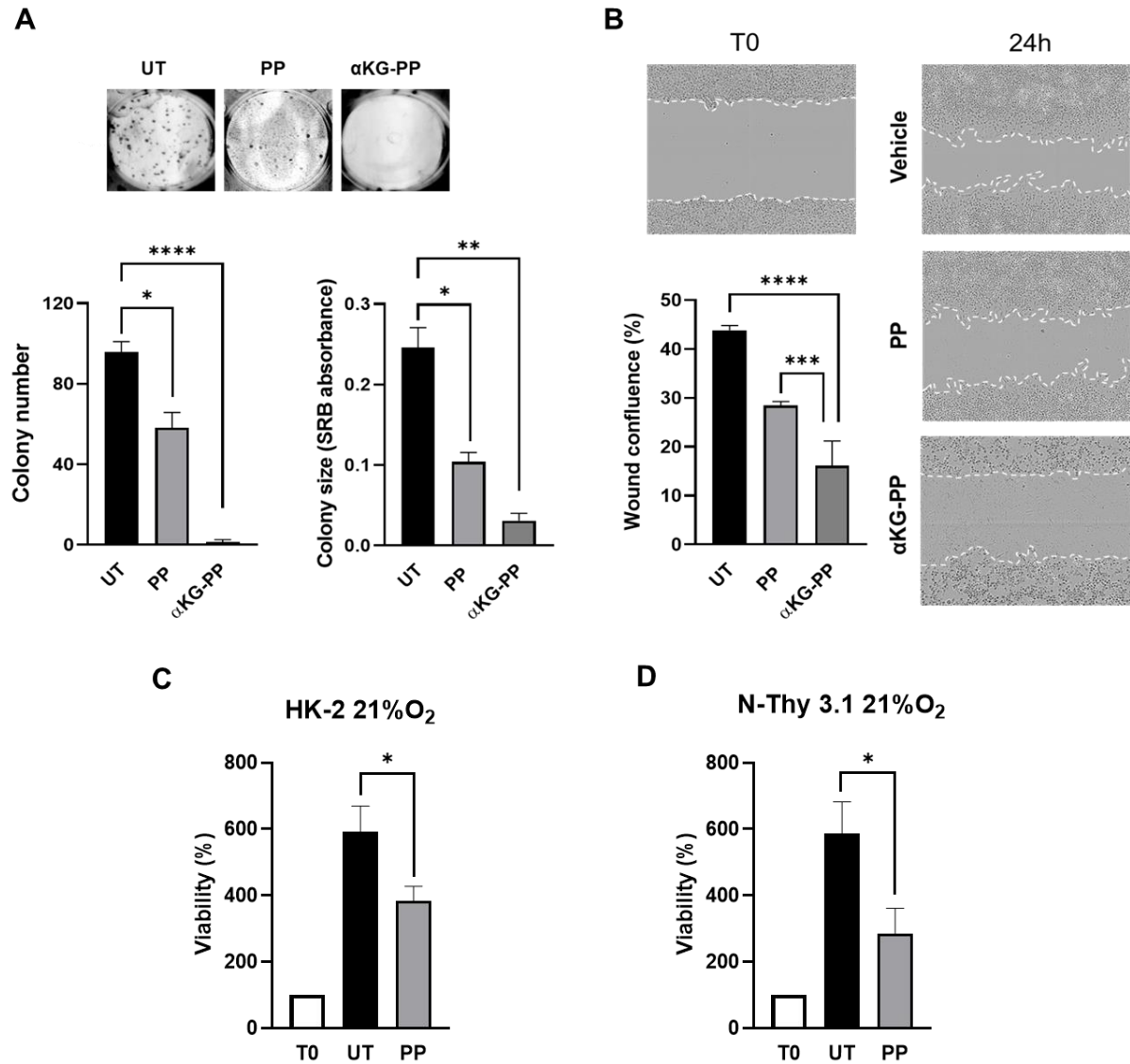


Figure 21: PP carrier *per se* displays a synergistic effect on kidney carcinoma cell migration properties. (A) Clonogenic abilities were determined in presence of 200 μ M α KG-PP or PP carrier for 7 days in low oxygen conditions (1% O₂). Colony number was counted, and colony size determined by SRB dye absorbance measured at 560 nm. A one-way ANOVA was performed for statistical analysis of data (mean \pm SEM) (n=3) * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$, **** $p \leq 0.0001$. (B) Cell migration in UOK-257 cells was evaluated through a wound-healing assay in presence of 200 μ M α KG-PP or PP carrier under high oxygen tension (21% O₂). Wound making was realised on cell monolayers at time 0 (T0) and wound closure monitored for 24h using Incucyte® S3 Live cell Analysis System. Wound confluence in UOK-257 monolayers (B) was calculated at experiment endpoint using Incucyte® S3 Live cell Analysis System Software. A one-way ANOVA was used for statistical analysis of data (mean \pm SEM) (n=3) * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$. (C-D) Cell viability of normal epithelial cells HK-2 (C) and N-Thy 3.1 (D) in high oxygen tension (21% O₂) was determined after 72h of treatment in presence of 200 μ M PP carrier using SRB assay. An unpaired t-test was used for statistical analysis of data (mean \pm SEM) (n=3). * $p \leq 0.05$

α KGlogue PP provokes α KG intracellular accumulation and imbalanced α KG/SA ratio

We previously described that CI-deficient cells are unable to stabilise HIF-1 α even in low oxygen tension as a result of PHDs chronic activation. At the metabolic level, these cells displayed increased α KG levels and reduced succinate reflecting a disrupted TCA cycle. To demonstrate that the selected α KG-PP permeates the cell membrane and causes increased α KG intracellular levels, LC-MS-based metabolomics analysis was carried out on UOK-257 cells after exposure to the compound for 1h and 3h. In these experiments, we used 2mM 3-methyl, 2-oxovaleric acid (KMV) to inhibit the α KG dehydrogenase complex (α KGDHC) and push the accumulation of endogenous as well as exogenous α KG, and we considered it as a positive control. UOK-257 cells incubated with 200 μ M α KG-PP for 1h or 3h showed a time-dependent increased levels of α KG (Figure 22A), reduced succinate levels (Figure 22B) correlating with an elevated α KG/succinate ratio (Figure 22C), while not altering 2-hydroxyglutarate (2-HG) levels (Figure 22D). In such context, the latter result indicates that, once uptaken, α KG is quickly metabolised by α KGDHC. Indeed, 2-HG levels rapidly increase when cells are treated with the combination of 200 μ M α K-PP and 2mM KMV (Figure 22D). Interestingly, the observed peak in α KG levels after 3 hours of treatment corresponds to reduced HIF-1 α abundance that is maintained even after 6 hours, while PP carrier has no effect at the same time points, thereby confirming that α KG-PP, and not the hydrophobic carrier, interferes with HIF-1 α stabilisation likely by activating prolyl hydroxylases (Figure 22E-F). Metabolomic analysis revealed that after 1 hour of incubation with α KG-PP only a slight decrease of glutamate was detected, while 3 hours post-treatment a consistent alteration of the TCA cycle was observed. Indeed, aconitate and glutamate levels were significantly reduced (Figure 23A, 23E), while fumarate and malate levels were increased (Figure 23C-D). Citrate and aspartate levels remained unchanged (Figure 23B, 23F). Interestingly, inhibition of α KGDHC by KMV pushes the TCA cycle to its extreme, inducing after just 1 hour a profound depletion of citrate, aconitate, glutamate and aspartate, while causing a striking accumulation of fumarate and malate (Figure 23A-F).

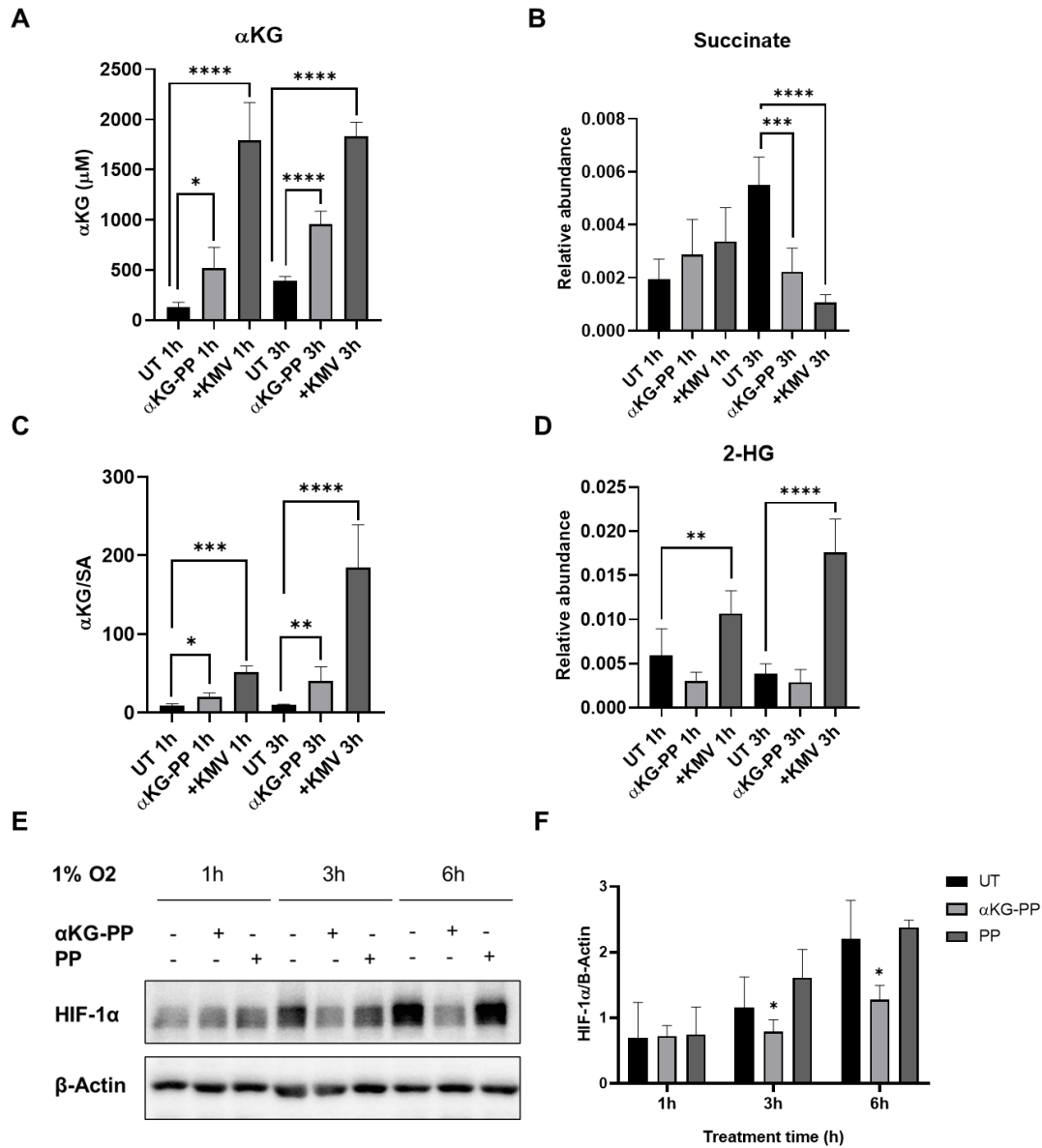


Figure 22: α KG-PP treatment triggered an increase of intracellular α KG correlated with HIF-1 α destabilisation in kidney carcinoma cells. (A) Intracellular α KG levels after 1 and 3 hours of exposure to 200 μ M α KG-PP were quantified using LC-MS approach under normoxia (21% O₂). To determine α KG intracellular levels, a calibration curve of the ketoacid was prepared and raw data normalised to mean cell volume. 3-methyl, 2-oxovaleric acid (KMV; 2mM) was used as a positive control for human α KGDH inhibition. (B) Succinate (SA) and 2-hydroxyglutarate (2-HG) (D) relative abundance values correspond to metabolites ion intensity normalised to internal standard Valine-d8. (C) α KG/SA ratio was calculated by the proportion of relative abundances of each metabolite. Metabolomics data (mean \pm SD) are representative of 6 technical replicates. A one-way ANOVA was performed for statistical analysis * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$, **** $p \leq 0.0001$. (E) Western blot analysis of HIF-1 α levels in UOK-257 cells untreated and treated with 200 μ M α KG-PP or PP carrier under hypoxia (1% O₂) for 1, 3 and 6 hours and respective densitometric quantification of protein levels reported to loading control β -actin (F). Data analysis (mean \pm SEM) (n=3) was carried out using a one-way ANOVA (mean \pm SEM). * $p \leq 0.05$

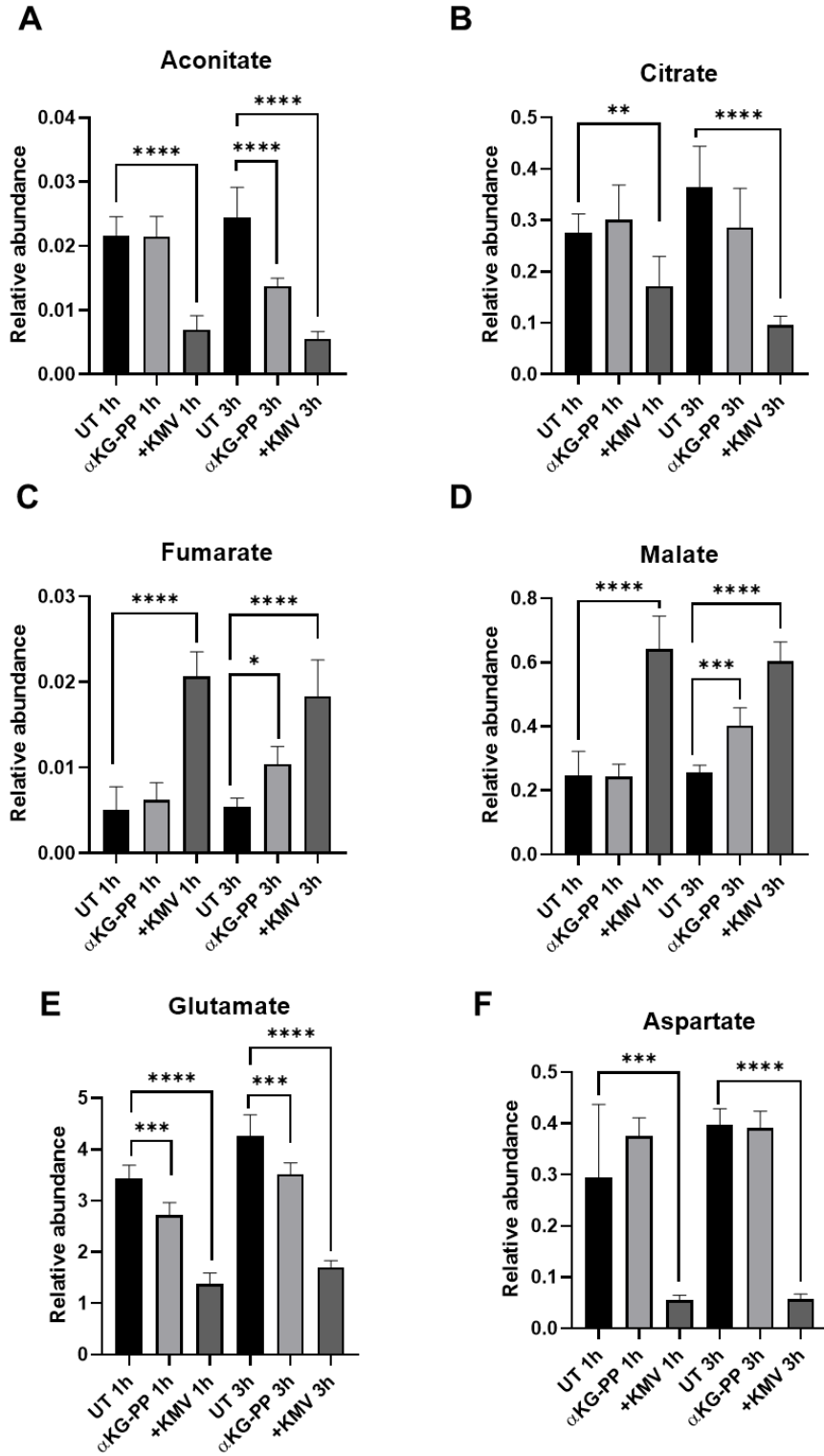


Figure 23: α KG-PP causes TCA cycle rewiring in kidney carcinoma cells. Relative abundance of aconitate (A), citrate (B), fumarate (C), malate (D), glutamate (E) and aspartate (F) were obtained after 3 hours of treatment under normoxia (21% O₂). Values correspond to metabolites ion intensity normalised to internal standard Valine-d8. Data (mean \pm SD), are representative of 6 technical replicates. A one-way ANOVA was performed for statistical analysis * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$, **** $p \leq 0.0001$.

The molecular mechanisms underlying α KG-PP effect imply the block of mTORC1 pathway

As reported in previous sections, α KG-PP and its corresponding carrier are capable of impairing cancer cell growth at high doses (200 μ M), and α KG-PP was much more potent in doing so. In this regard, and with the aim to investigate the modalities underlying the effect of α KG-PP on UOK-257 cell viability, we started by exploring apoptosis induction resulting from α KG-based treatment as previously reported in literature (Tennant and Gottlieb 2010). In this regard, DAPI-stained nuclear structures of untreated UOK-257 cells or treated with either α KG-PP or PP carrier did not show any sensitive alterations or apoptotic features up to 72h of treatment in normoxia (21% O₂) (Figure 24A) nor in hypoxia (1% O₂) (data not shown) thereby eliminating a hypothetical apoptotic cell death that would be due to α KG-PP or corresponding carrier. Furthermore, a flow cytometry analysis was performed on UOK-257 cells 72h post-treatment with 200 μ M of α KG-PP or PP carrier in normoxia (21% O₂), using Annexin V (AV) as a marker for apoptotic cell death along with propidium iodide (PI). Both experiment and analysis were carried out in high oxygen tension since flow cytometer does not allow a controlled oxygen supply in order to maintain cells under low oxygen conditions. At the experiment endpoint, results revealed a shift in cell populations. While the untreated condition counted around 89% of live cells, this percentage was of 86.3% in cells treated with PP carrier and to 82.9% in α KG-PP-treated cells (Figure 24B). In this latest condition, the proportion of dead cells was twice as much as in the untreated control (5.73%) with 12.5% dead cells, while 200 μ M PP provoked 8.70% cell death (Figure 24B). These data thus support cell viability experiments previously described, showing that α KG-PP induces cell death on the one hand and confirming the contribution of PP carrier. However, it is worth to note that the proportion of dead cells induced by the analogue in this last case was less marked than in SRB viability assay. Moreover, the induction of senescence in these cells was also investigated. In this frame, treated and untreated kidney carcinoma cells stained negative to senescence-specific β -galactosidase assay (Figure 24C, *upper panel*) 72h after treatment with either 200 μ M of α KG-PP or PP carrier in normoxia, thus ruling out this pathway as a possible mechanistic consequence of α KG accumulation. Similarly, no differences in LC-3 protein levels or processing were observed up to 6h of treatment with α KG-PP or PP carrier in hypoxia (Figure 24C, *lower panel*) excluding the induction of autophagy as a consequence of α KG accumulation at least not as an early event during treatment.

Being a precursor of glutamine, α KG is tightly involved in amino acids metabolism. On the other hand, mammalian Target of Rapamycin Complex 1 (mTORC1), constitutes the master regulator of protein synthesis in response to nutrients availability and proliferation needs of rapidly growing cancer cells (Saxton and Sabatini 2017). Interestingly, analysing proteins of this pathway through western blot in a context of α KG accumulation surprisingly revealed treatment with α KG-PP and not PP carrier correlated with an inhibition of mTORC1 pathway after 1, 3 and 6 hours in hypoxia. Indeed, Raptor, one of mTORC1 associated regulatory proteins necessary for the complex binding to its targets, was phosphorylated at Serine 792 only in samples treated with α KG-PP (Figure 24D), highlighting the protein inactivation and thus the shut-off of mTORC1 signalling. Next to that, no notable differences in total or phosphorylated mTOR levels were observed (Figure 24D). Such results thus suggest increased intracellular α KG levels in UOK-257 cells correlate with a rapid inhibition of mTORC1 signalling. Furthermore, the phosphorylated forms of p70S6K and 4E-BP1, two downstream substrates of mTORC1 involved in the initiation of cap-dependent translation and protein synthesis, were notably reduced in UOK-257 cells exposed to α KG-PP for 48h with respect to the untreated (Figure 24E), indicating α KGlogue PP represses mTORC1 signalling and protein synthesis at 48h in low oxygen tension while no such effect was notable at earlier times, namely 16 and 24h of treatment. Surprisingly, PP carrier also appeared to downmodulate mTORC1 pathway in UOK-257 cells after 48h, although less marked than the analogue itself, suggesting once more an additive effect of the carrier in this context (Figure 24E). Notably, total and phosphorylated mTOR levels remained unchanged between 16h to 48h of treatment (Figure 24E).

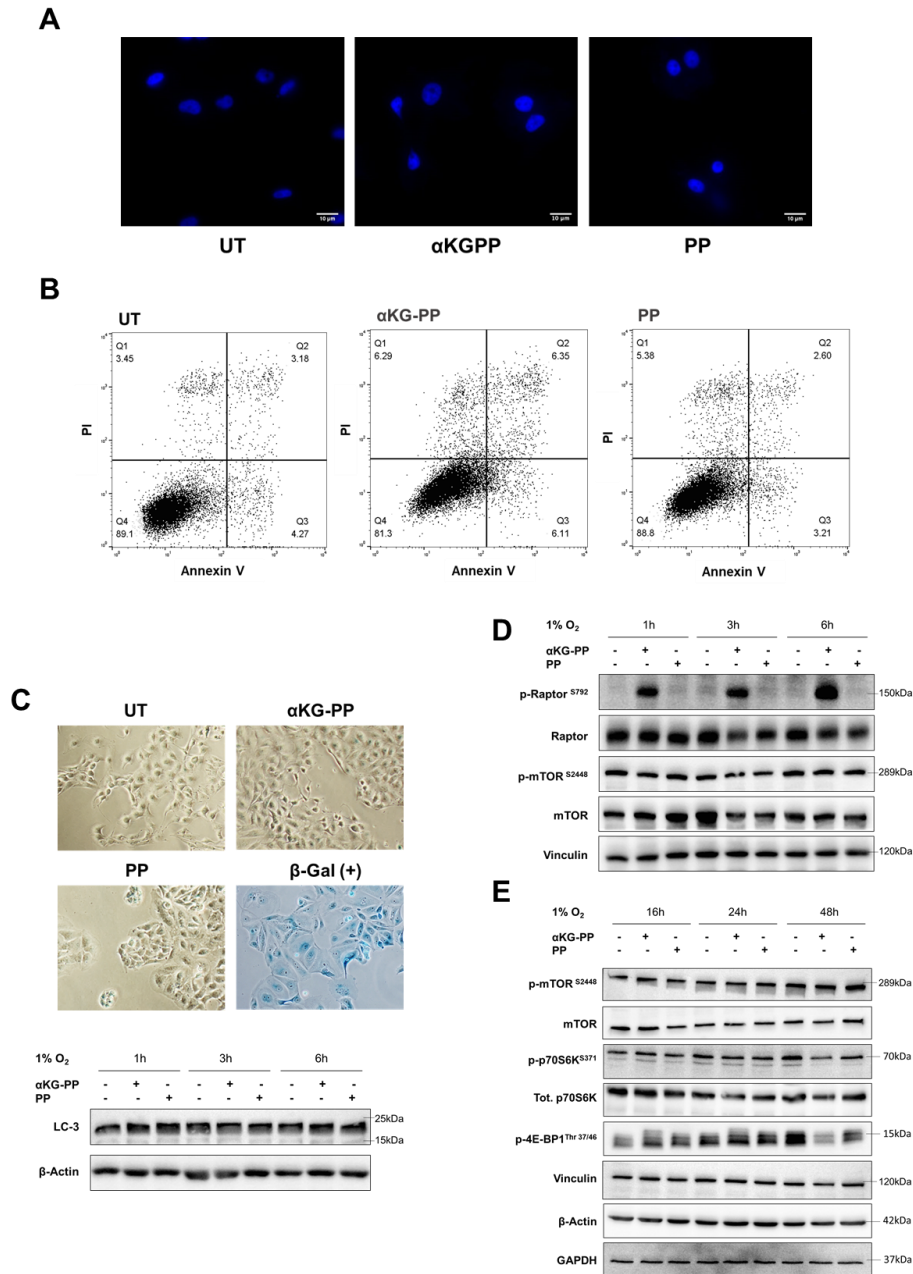


Figure 24: Molecular mechanisms underlying αKG-PP effect in UOK-257 cells imply the block of protein synthesis via mTORC1 signalling. (A) Nuclei morphology was visualized by DAPI staining upon exposure to 200μM αKG-PP and PP carrier for 72h under normoxia (21% O₂). (B) Apoptotic death was evaluated using PI and AV as markers in flow cytometry after 72h of αKG-PP and PP treatment under normoxia (21% O₂). (C), Senescence-specific β-galactosidase staining of UOK-257 cells untreated or treated with 200μM αKG-PP and PP for 72h under normoxia (21% O₂) (*upper panel*). Western blot analysis of autophagy marker LC-3 up to 6h of treatment with αKG-PP and PP under hypoxia (1% O₂) (*lower panel*). (D, E) Western blot analysis of mTOR pathway at different times of treatment with αKG-PP and PP under hypoxia (1% O₂).

α KG-PP displays anti-proliferative properties in cancer-derived spheroids and *in vivo*

At this stage, we aimed at translating the use of α KG-PP in more complex models such as 3D cultures and animal models. Hence, multicellular spheroids derived from TPC-1 and UOK-257 cells were generated in ULA plates. The obtained 3D models of approximately 200 μ m diameter were described to recapitulate several properties (oxygen and nutrients gradient, heterogenous cell population) of solid tumors *in vivo*. Spheroids were consequently treated with 200 μ M α KG-PP, while 200nM staurosporine (STS) was used as a positive control. In this regard, results revealed that the two tested models treated with α KG-PP showed no difference in the proportion of dead cells compared to the untreated control (Figure 25A-B) after 3 days of treatment, while 200nM STS induced a significant cell death. It is possible that at this dose, a treatment duration of 3 days is too short to see any effect on the growth of complex structures such as spheroids. Consequently, treatment was extended to longer periods, as most reports in literature often refer to 7 days as a mean duration. A subsequent experiment in which UOK-257-derived spheroids were maintained in presence of α KG-PP for 7 days confirmed the absence of significant differences in spheroids size 3 days post-treatment (Figure 25C), whereas at day 7 the 3D cancer model exposed to α KG-PP and PP carrier looked significantly smaller in size compared to the untreated control (Figure 25C). These data are comforted by an MTT viability assay that showed the proportion of metabolically active cells was significantly lower in spheroids exposed to 200 μ M α KG-PP compared to untreated control. Moreover, the percentage of viable cells in presence of α KG-PP was 50% less than in spheroids exposed to PP carrier after 7 days of treatment (Figure 25C). Hence, these preliminary data strongly corroborate an anti-proliferative effect of α KG-PP in the 3D kidney cancer model as well as a synergistic action of the PP carrier in this model.

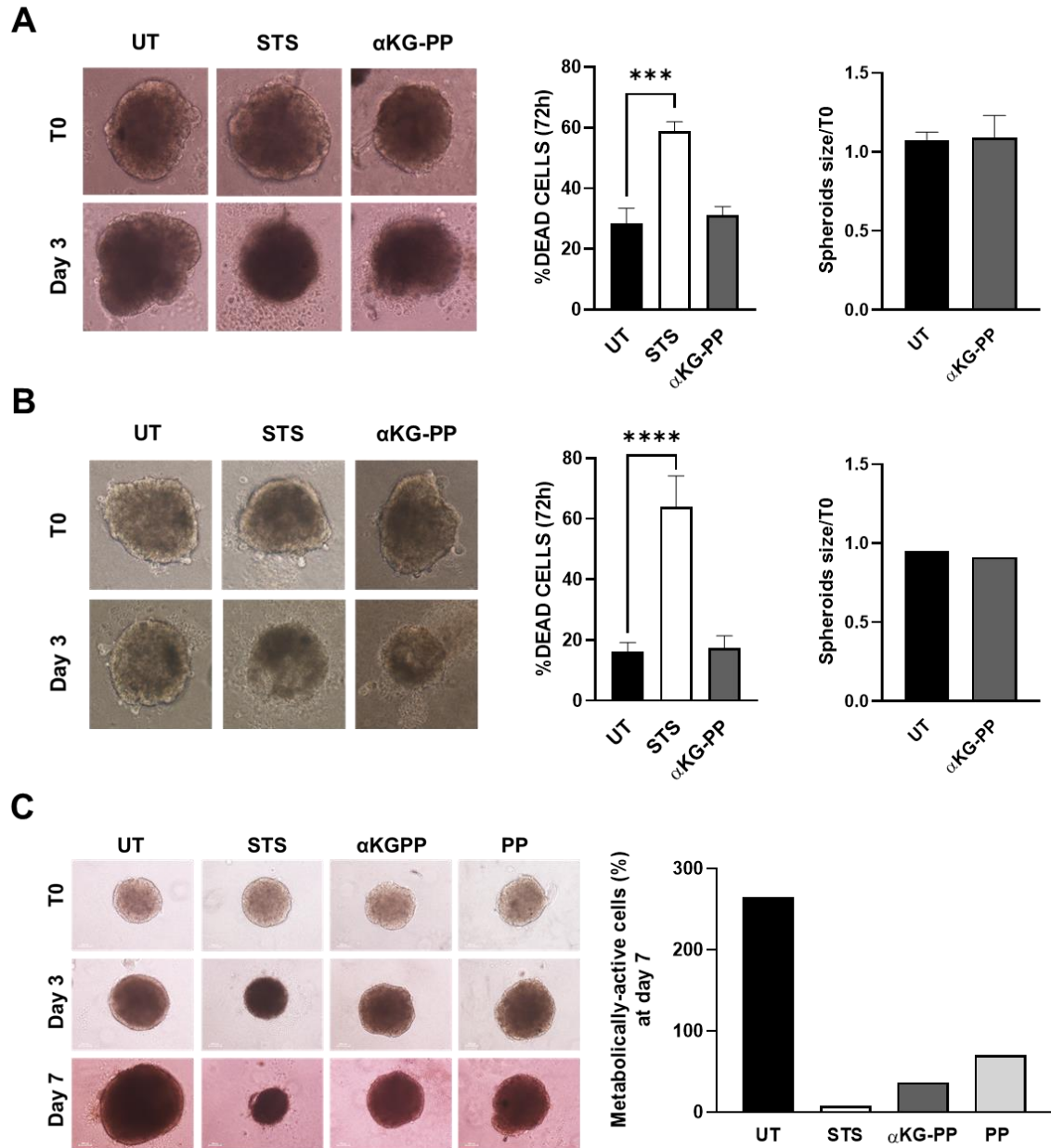


Figure 25: αKG-PP alters 3D spheroids size and viability. Size and cytotoxicity assessment in UOK-257 (A) and TPC-1-derived spheroids (B) after 3 days of treatment with 200μM αKG-PP. 200nM staurosporine (STS) was used as a positive control. Quantitative analysis of dead cells was determined using Promega's CytoTox-Glo™ bioluminescence assay. A one-way ANOVA was used for statistical analysis of data (mean ± SEM, n≥4) * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$. Spheroids size (mean ± SD) was measured using ImageJ free software (NIH) and normalised to their size at Time 0. (C) Growth of UOK-257-derived spheroids up to 7 days of treatment (n=1) with 200μM αKG-PP and PP carrier. Percentage of viable cells at day 7 in UOK-257-derived spheroids was determined using MTT assay. Data were normalised to viable cells at time 0 considered as 100% (n=1).

Drosophila melanogaster is considered a handful *in vivo* model to study the complex features of cancer thanks to signaling pathways and regulatory system preservation from human to flies (Mirzoyan et al., 2019). The use of specific and advanced genetic tools and its short life cycle (10 days at 25°C) make flies easy to manipulate. *Drosophila* is also an excellent model for drug screening studies because, in addition to closely reproducing the typical human cancer traits, it allows the analysis of a large number of individuals. To investigate the consequence of α KG-PP treatment *in vivo*, tumor growth in the dorsal compartment of imaginal wing discs was induced. 6 days after egg laying (AEL) tumor individuals were selected and exposed to 200 μ M α KG-PP for 2 days. Wing disc isolation revealed a 34% decrease in tumor size of treated individuals with respect to the untreated counterpart as highlighted by volume analysis (Figure 26). These preliminary data thus confirm α KG-PP potency to slowdown tumor growth *in vivo*. However, whether the analogue-mediated effect in *Drosophila* wing discs is due to increased cell death or to reduced proliferation remains to be determined.

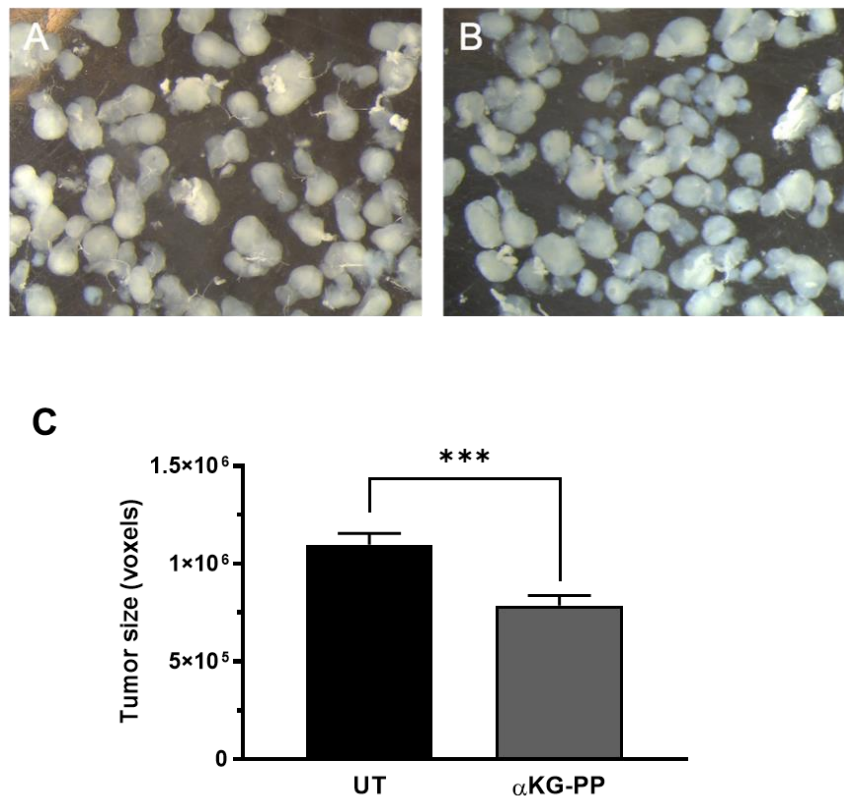


Figure 26: α KG-PP displays antiproliferative properties *in vivo*. Tumors isolated from ap-*lgl*^{KD}, *Ras*^{V12} untreated samples (A) or treated with 200 μ M α KG-PP (B) for 2 days. (C) Volume analysis of ap-*lgl*^{KD}, *Ras*^{V12} tumor samples untreated (n=46) and treated with α KG-PP analogue (n=48). An unpaired t-test was used for statistical analysis ***p \leq 0.001

DISCUSSION

Targeting hypoxic adaptation in cancer has long constituted an attractive approach to tackle tumor progression. Although focused approaches as represented by HIF inhibitors seem to constitute an interesting alternative, their use as single therapies in cancer patients is seriously limited by the high resistance rates and relapse. For this reason, now more than ever, the perspective of combining classical chemotherapy/radiotherapy to emerging complementary approaches among which targeting metabolism and hypoxia adaptation appears to be more convenient to enhance the chances of treatment success and are consequently being investigated in clinical trials.

Here, we propose an adjuvant and safe metabolic-based therapeutic approach taking into account that TCA metabolites may also act as tumor growth modulators. In this framework, we have previously demonstrated that a severe mitochondrial CI impairment triggers an increase of both NADH/NAD⁺ and α KG/SA ratio, causing chronic HIF-1 α degradation (*pseudonormoxia*) and in turn, tumor growth arrest (Porcelli et al., 2010) (Gasparre et al., 2011) (Calabrese et al., 2013) (Iommarini et al., 2014) (Kurelac et al., 2019). To recapitulate this low-proliferative phenotype we exploited the use of cell-permeable α KGlogues to provoke the increase of the physiological substrate of PHDs feeding their activity. Indeed, it is well known that the slightest fluctuations in α KG levels feeds the PHDs reaction (K_m around 50 μ M). Hence, we generated a panel of 7 novel α KGlogues that maintain their structural integrity both in organic solvents and in aqueous solution. We screened the analogues, to assess their ability to stimulate HIF-1 α degradation under hypoxic conditions and to consequently impair cancer cells proliferation without exerting broad cytotoxicity on non-cancer controls. Consequently, only the most selective compounds displaying the least toxic side-effects on the non-cancer cells were considered for further investigations.

Surprisingly, testing the 7 analogues on thyroids carcinoma (TPC-1) and kidney carcinoma (UOK-257) cell lines revealed different sensitivities in terms of HIF-1 α degradation. We observed that while TPC-1 cells responded more to 200 μ M of α KG-tB, α KG-N, α KG-Cl, α KG-L and α KG-G, UOK-257 cells were more sensitive to α KG-PP, α KG-Cl, α KG-P, α KG-N and α KG-G, to a lesser extent. Such a disparity between the two cancer cell models may be attributed to each cell respective membrane composition, which make them more permeable to some analogues harbouring specific hydrophobic groups and less to others. In this regard, the commercial α KG-DM is unable to influence HIF-1 α expression levels which remained as high as the untreated control in UOK-257 cells whereas the same dose of compound significantly reduced HIF-1 α abundance 60 and 90 minutes after exposure in TPC-1 cells.

Such results thus suggest UOK-257 cells membrane permeability is more selective compared to TPC-1. Moreover, the rate of delivery and use of the compounds which likely varies from one cell to another based on their metabolic profile could strongly influence the analogues intracellular kinetics. This can account for the transient effect observed with α KG-N and α KG-P in UOK-257 cells suggesting these compounds have a short half-life and possibly they are quickly metabolized following cell uptake. Indeed, in a study carried out by Tennant and collaborators, the authors reported a peak in α KG intracellular levels as early as 45 minutes following α KG-analogues administration, after which the metabolite's concentration rapidly decreased to reach the baseline at 120 minutes. Interestingly, structure optimisation of monoester T α KG to produce diester ET α KG was able to prolong α KG accumulation inside the cells up to 4h thereby directly linking the analogues structure with their ability to maintain steady delivery of α KG to the cell (Tennant et al., 2009). It is worth to add that in our tested cancer cell models, un-conjugated α KG was unable to affect HIF-1 α protein levels under hypoxic conditions further confirming similar observations by Gottlieb and his group (MacKenzie et al., 2007; Tennant et al., 2009) who showed free α KG inability to cross the plasma membrane as reflected by unchanged metabolite's intracellular levels.

In light of the screening results, we were able to select 4 analogues on the thyroid carcinoma cell line namely, α KG-N, α KG-L, α KG-tB and α KG-Cl, and 5 for the kidney carcinoma cells (α KG-G, α KG-N, α KG-Cl, α KG-P and α KGPP), based on their respective abilities to induce HIF-1 α degradation under hypoxic conditions. Next, we investigated the effect of the selected compounds on cancer cells proliferation in a context of HIF-1 α destabilisation. In this regard, 200 μ M α KG-G, α KG-N and α KG-L showed little or no effect on the proliferation of thyroid carcinoma cells (TPC-1) nor on the non-cancer thyroid epithelial cells (N-Thy 3.1) up to 72h under hypoxic condition. Similarly, we noted that α KG-G and α KG-N or α KG-P were unable to affect the growth of the kidney cell models up to 200 μ M independently from oxygen conditions. These analogues showed a transient effect on HIF-1 α protein expression which was recovered after 90 minutes of treatment, potentially hinting that the compounds display an early biological effect on HIF-1 α protein levels which is overcome due to the fast use of the metabolite. Interestingly, in the literature α KG analogues were reportedly used at concentration ranging from 2mM to 5mM, albeit at least 10 times more than in the present study. In light of PHDs affinity for their substrate (K_m around 50 μ M), this might account for the low potency of doses as small as 2 μ M and 20 μ M which maybe too weak to influence the

hydroxylases activity, further highlighting the necessity to use doses at least equal or superior to α KG physiological levels in order to observe a biological effect.

In addition, we show that α KG-Cl displayed a dose-dependent effect on the proliferation of both TPC-1 and UOK-257 cells with doses as low as 2 μ M ultimately resulting in a blocked proliferation at 200 μ M independently of oxygen tension, suggesting the analogue's effect on cell growth is likely independent from HIF-1 α status. Such an observation could be due to an off-target effect or attributed to the activity of the hydrophobic carrier *per se*. Overall, despite being well tolerated by the epithelial kidney cells, this analogue severely hampered the growth of the non-cancer thyroid cells at 200 μ M and was therefore discarded from the study. These results highlight the sensitivity to different treatments is strongly related to the cells tissue of origin, a parameter often recognised to further complicate the development of anti-cancer therapies.

Although it is well known that coupling α KG to hydrophobic groups enhances its membrane permeability, however, the possibility that these carriers alone, may display a biological activity cannot be excluded. In this regard, we show that α KG-tB selectively hampered the growth thyroid carcinoma cells and *in vitro* tumorigenic properties at 200 μ M without inducing marked toxicity on the non-cancer N-Thy 3.1 cells up to 72h of treatment. However, despite its high potency in recreating a *pseudonormoxic* state up to 12h of exposure (Figure 18A-C) we were able to demonstrate that the anti-proliferative effect of α KG-tB on the thyroid cancer cells was independent from HIF-1 α destabilisation and is, instead solely due a non-specific activity of the hydrophobic carrier tB, thereby leading to its exclusion. Hence, at the term of the screening phase and based on each analogue's effectiveness and safety properties which constituted our main criteria in this study, α KG-PP was selected as the most promising hit and all the other analogues were discarded.

Indeed, the potential of α KG-PP lied in its ability to impair the growth of the kidney carcinoma cells at 200 μ M ultimately leading to cell death with good safety levels on the kidney epithelial counterparts under hypoxic conditions, overall correlating with a sustained HIF-1 α destabilisation at long term and the repression of cancer cells *in vitro* clonogenic and migration abilities. Further, taking advantage of HIF-TM overexpressing cells, we were able to establish a direct link between α KG-PP treatment, HIF-1 α expression and altered cancer cells growth. We demonstrated that the growth alteration provoked by α KG-PP in UOK-257 cells is in part dependent on blocked HIF signalling, the other part being due to a synergistic

activity of the PP carrier independently from HIF-1 α status. To our knowledge, this is the first time the single activity of the carriers is reported unveiling an additive effect on cancer cells growth and tumorigenic properties. We provide evidence that exposure to α KG-PP and not PP carrier specifically blocked HIF-1 α stabilisation in UOK-257 cells. At the intracellular level, this correlated with a peak in α KG concentration 1 and 3h post-treatment culminating in increased α KG/SA ratio. Consistently with former studies, these data give further insight at two levels: first by confirming the ability of our synthesised analogue to permeate through the plasma membrane and cause the accumulation of the ketoacid inside the cells (Mackenzie et al., 2007; Tennant et al., 2009). On the other hand, and as previously emphasized, a high α KG/SA is one of the main features of CI-deficient cells thus confirming our initial hypothesis that α KG supplementation is able to recapitulate some features of CI-deficient cells, namely a high α KG /SA ratio together with chronic HIF-1 α destabilisation.

Besides α KG accumulation, metabolomics data revealed oncometabolite 2-HG levels remained stable 3h post-treatment indicating that the exogenous α KG is quickly metabolised. On the other hand, the low levels of SA coupled to an increased malate/aspartate ratio, a direct indicator of NADH accumulation, hint to the reduction in the oxidative flux of the TCA cycle usually endorsed by α KGDHC. Indeed, the activity of the enzymatic complex is known to be negatively regulated by increased NADH/NAD⁺, especially in a context of severe mitochondrial defects (Calabrese et al., 2013) (Vatrinet et al., 2017). However, further analysis is likely warranted to clearly sustain these observations. At the metabolic level, other works reported ester analogues of the ketocid to reverse the glycolytic profile characterising hypoxic cancer cells, by reducing their glucose consumption and lactate production *in vitro* and *in vivo* to finally converge in PHD3-mediated apoptotic cell death (Tennant et al., 2009) (Tennant and Goettlieb 2010). Independently of HIF-1 α and far from its effect in a hypoxic context, α KG-DM, a commercial ester analogue, was recently reported to induce synthetic lethality in a panel of cancer cells when combined to a well-known OXPHOS inhibitor, namely BAY87-2243. In addition to blocking oxidative phosphorylation, the drug combination displayed a synergistic effect to suppress glycolysis through a mechanism involving MDM2 transcriptional response culminating in a bioenergetic crisis and triggering cell death in a panel of cancer cell models (Sica et al., 2019). More recently, a strong line of evidence highlights the anti-tumorigenic activity of the ketoacid mediated through the stimulation of other dioxygenases of the α KGDDs family, namely DNA and histone demethylases TETs and KDMs ultimately reversing pro-tumorigenic epigenetic signals. In

this regard, α KG-DM was described to recapitulate p53 transcriptional response and favour cell differentiation via the reactivation of TETs enzymes in a model of pancreatic ductal adenocarcinoma (Morris et al., 2019).

In our hands, although UOK-257 exposure to α KG-PP or PP carrier induced a cytotoxic cell death, cells showed no morphological features of apoptosis, thus indicating the analogue and carrier anti-proliferative activity is mediated through a different mechanism. Similarly, α KG-PP did not trigger senescence nor autophagy in the kidney carcinoma cells. Instead, the supplementation of the ketoacid seemed to mediate a rapid repression of mTORC1 signalling. These data suggest that in addition to inducing a state of *pseudonormoxia*, the intracellular accumulation of α KG secondary to treatment also correlated with the inhibition of mTOR signalling, potentially accounting for the growth arrest observed in these cells. Interestingly, mTOR signalling cascade is well known to act upstream of HIF-1 α thereby promoting *HIF1A* mRNA transcription and translation (Iommarini et al., 2017). Hence, by downmodulating mTORC1 pathway, it is possible that exogenous α KG indirectly potentiates its repressive activity on HIF-1 α expression. In addition, preliminary data at longer terms revealed that α KG-PP-mediated mTORC1 repression is maintained over time and in such a context, PP carrier *per se* also appeared to contribute to the downregulation of the mitogenic pathway further confirming its synergistic activity on cell growth as previously related. Analogous effects were described during the response to pro-apoptotic and cytotoxic compounds like staurosporine, which reportedly inhibited mTOR-dependent protein synthesis by directly acting on its downstream targets (Tee and Proud 2001). Similarly to staurosporine, treatment with α KG was shown to impair the proliferation of colon adenocarcinomas cell lines by inducing cell cycle arrest in normoxia (Rzeski et al., 2012). It is therefore possible that α KG-PP and PP carrier block cell cycle progression by inactivating mTOR downstream targets and shutting down protein synthesis to finally trigger cell death. In this regard, α KG accumulation may induce an immediate cell death following the double repression of HIF-1 α and mTOR signalling while the PP carrier may provide a late additive effect thereby sustaining cell death. Nevertheless, further investigations are ongoing to confirm the previous observations and clearly determine the mechanisms underlying α KG-PP and PP carrier anti-proliferative activity in other cancer cell models.

To conclude, the pleiotropic implication of the metabolite highlights its multiple targets and thus considerably widens the scope of its therapeutic applications. This study sustains previous reports in shedding light on the great potential α KG holds to modulate cancer

progression. At the present time, no clinical studies have included α KG as a therapeutic agent in the context of cancer and studies have been restricted to murine models so far. On the other hand, thanks to the preservation of signaling pathways from human to flies and their facility of use, *Drosophila* constitutes an excellent model for drug screening studies. In this regard, our preliminary data confirmed the anti-proliferative activity of α KG-PP *in vivo* on a *Drosophila* cancer model thereby strengthening the anti-tumorigenic potential of α KG analogues and paving the way to further studies. The encouraging results presented herein along with those increasingly reported in literature support the hypothetic anti-cancer activity of the ketoacid and open the possibility to the application of an α KG-based therapy in combination with conventional or novel chemotherapeutic drugs in the frame of a synthetic lethality approach, however, before considering the translation in cancer patients in the clinic the candidate analogues would priorly need to be validated through pre-clinical studies.

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